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<p>(54) Title: DNA SEQUENCES, RECOMBINANT DNA MOLECULES AND PROCESSES FOR PRODUCING SOLUBLE T4 PROTEINS</p>		
<p>(57) Abstract</p> <p>This invention relates to DNA sequences, recombinant DNA molecules and processes for producing soluble T4 protein. More particularly, this invention relates to DNA sequences that are characterized in that they code on expression in an appropriate unicellular host for soluble forms of T4, the receptor on the surface of T4+ lymphocytes, or derivatives thereof. In accordance with this invention, the DNA sequences, recombinant DNA molecules and processes of this invention may be employed to produce soluble T4 essentially free of other proteins of human origin. This soluble protein may then advantageously be used in the immunotherapeutic and diagnostic compositions and methods of this invention. The soluble T4-based immunotherapeutic compositions and methods of this invention are useful in treating immunodeficient patients suffering from diseases caused by infective agents whose primary targets are T4+ lymphocytes. According to a preferred embodiment, this invention relates to soluble T4-based compositions and methods which are useful in preventing, treating or detecting acquired immune deficiency syndrome, AIDS related complex and HIV infection.</p>		

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**DNA SEQUENCES, RECOMBINANT DNA MOLECULES  
AND PROCESSES FOR PRODUCING SOLUBLE  
T4 PROTEINS**

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**TECHNICAL FIELD OF INVENTION**

This invention relates to DNA sequences, recombinant DNA molecules and processes for producing soluble T4 proteins. More particularly, this invention relates to DNA sequences that are characterized in  
10 that they code on expression in an appropriate unicellular host for soluble forms of T4, the receptor on the surface of T4<sup>+</sup> lymphocytes, or derivatives thereof. In accordance with this invention, the DNA sequences, recombinant DNA molecules and processes  
15 of this invention may be employed to produce soluble T4 essentially free of other proteins of human origin. This soluble protein may then advantageously be used in the immunotherapeutic, prophylactic, and diagnostic compositions and methods of this invention.

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The soluble T4 protein-based immunotherapeutic compositions and methods of this invention are useful in treating immunodeficient patients suffering from diseases caused by infective agents whose primary targets are T4<sup>+</sup> lymphocytes. According to a  
25 preferred embodiment, this invention relates to soluble T4 protein-based compositions and methods which are useful in preventing, treating or detecting

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acquired immune deficiency syndrome, AIDS related complex and HIV infection.

#### BACKGROUND ART

The class of immune regulatory cells known  
5 as T cell lymphocytes can be divided into two broad functional classes, the first class comprising T helper or inducer cells -- which mediate T cell proliferation, lymphokine release and helper cell interactions for Ig release, and the second class comprising  
10 T cytotoxic or suppressor cells -- which participate in T cell-mediated killing and immune response suppression. In general, these two classes of lymphocytes are distinguished by expression of one of two surface glycoproteins: T4 (m.w. 55,000-62,000  
15 daltons) which is expressed on T helper or inducer cells, probably as a monomeric protein, or T8 (m.w. 32,000 daltons) which is expressed on T cytotoxic or suppressor cells as a dimeric protein.

The primary structures of T4 and T8 have  
20 been deduced from their respective cDNA sequences [P. J. Maddon et al., "The Isolation and Nucleotide Sequence Of A cDNA Encoding The T Cell Surface Protein T4: A New Member Of The Immunoglobulin Gene Family", Cell, 42, pp. 93-104 (1985); D. R. Littman et al.,  
25 "The Isolation And Sequence Of The Gene Encoding T8: A Molecule Defining Functional Classes Of T Lymphocytes", Cell, 40, pp. 237-46 (1985)]. Both predicted protein sequences define molecules with domains expected for surface antigens, including transmembrane and intracytoplasmic domains at the carboxyl  
30 end of the protein. In addition, both proteins contain an amino terminal region which shows striking homology to immunoglobulin and T cell receptor variable regions and which might function during  
35 target cell recognition [Maddon et al., supra].

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In immunocompetent individuals, T4 lymphocytes interact with other specialized cell types of the immune system to confer immunity to or defense against infection [E. L. Reinherz and S. F. Schlossman, "The Differentiation Function Of Human T-Cells", Cell, 19, pp. 821-27 (1980)]. More specifically, T4 lymphocytes stimulate production of growth factors which are critical to a functional immune system. For example, they act to stimulate B cells, the descendants of hemopoietic stem cells, which promote the production of defensive antibodies. They also activate macrophages ("killer cells") to attack infected or otherwise abnormal host cells and they induce monocytes ("scavenger cells") to encompass and destroy invading microbes.

It has been found that the primary target of or receptor for certain infective agents is the T4 surface protein. These agents include, for example, viruses and retroviruses. When T4 lymphocytes are exposed to such agents, they are rendered nonfunctional. As a result, the host's complex immune defense system is destroyed and the host becomes susceptible to a wide range of opportunistic infections.

Such immunosuppression is seen in patients suffering from acquired immune deficiency syndrome ("AIDS"). AIDS is a disease characterized by severe or, typically, complete immunosuppression and attendant host susceptibility to a wide range of opportunistic infections and malignancies. In some cases, AIDS infection is accompanied by central nervous system disorders. Complete clinical manifestation of AIDS is usually preceded by AIDS related complex ("ARC"), a syndrome accompanied by symptoms such as persistent generalized lymphadenopathy, fever and weight loss. The human immunodeficiency virus ("HIV") retrovirus is thought to be

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the etiological agent responsible for AIDS infection and its precursor, ARC [M. G. S. rmgadharan et al., "Detection, Isolation And Continuous Production Of Cytopathic Retroviruses (HTLV-III) From Patients With AIDS And Pre-AIDS", Science, 224, pp. 497-508 (1984)].\*

Between 85 and 100% of the AIDS/ARCS population test seropositive for HIV [G. N. Shaw et al., "Molecular Characterization Of Human T-Cell Leukemia (Lymphotropic) Virus Type III In The Acquired Immune Deficiency Syndrome", Science, 226, pp. 1165-70 (1984)]. The number of adults in the United States infected with HIV has been estimated to be between 1 and 2.5 million [D. Barnes, "Strategies For An AIDS Vaccine", Science, 233, pp. 1149-53 (1986); M. Rees, "The Sombre View Of AIDS", Nature, 326, pp. 343-45 (1987)]. These estimates include 64,900 individuals who do not belong to an identified group at risk for AIDS [S. L. Sivak and G. P. Wormser, "How Common Is HTLV-III Infection In The United States?", New Eng. J. Med., 313, p. 1352 (1985)]. The apparent annual rate of diagnosis for those infected with HIV virus is between 1 and 2% -- a rate which may increase significantly in future years.

The genome of retroviruses, such as HIV, contains three regions encoding structural proteins. The gag region encodes the core proteins of the virion. The pol region encodes the virion RNA-dependent DNA polymerase (reverse transcriptase). The

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\* In this application, human immunodeficiency virus ("HIV"), the generic term adopted by the human retrovirus subcommittee of the International Committee On Taxonomy Of Viruses to refer to independent isolates from AIDS patients, including human T cell lymphotropic virus type III ("HTLV-III"), lymphadenopathy-associated virus ("LAV"), human immunodeficiency virus type 1 ("HIV-1") and AIDS-associated retrovirus ("ARV") will be used.

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env region encodes the major glycoprotein found in the membrane envelope of the virus and in the cytoplasmic membrane of infected cells. The capacity of the virus to attach to target cell receptors and to  
5 cause fusion of cell membranes are two HIV properties controlled by the env gene. These properties are believed to play a fundamental role in the pathogenesis of the virus.

HIV env proteins arise from a precursor  
10 polypeptide that, in mature form, is cleaved into a large heavily glycosylated exterior membrane protein of about 481 amino acids -- gp120 -- and a smaller transmembrane protein of about 345 amino acids which may be glycosylated -- gp41 [L. Ratner et al.,  
15 "Complete Nucleotide Sequence Of The AIDS Virus, HTLV-III", Nature, 313, pp. 277-84 (1985)].

The host range of the HIV virus is associated with cells which bear the surface glycoprotein T4. Such cells include T4 lymphocytes and  
20 brain cells [P. J. Maddon et al., "The T4 Gene Encodes The AIDS Virus Receptor And Is Expressed In The Immune System And The Brain", Cell, 47, pp. 333-48 (1986)]. Upon infection of a host by HIV virus, the T4 lymphocytes are rendered non-functional. The  
25 progression of AIDS/ARCS syndromes can be correlated with the depletion of T4<sup>+</sup> lymphocytes, which display the T4 surface glycoprotein. This T cell depletion, with ensuing immunological compromise, may be attributable to both recurrent cycles of infection and  
30 lytic growth from cell-mediated spread of the virus. In addition, clinical observations suggest that the HIV virus is directly responsible for the central nervous system disorders seen in many AIDS patients.

The tropism of the HIV virus for T4<sup>+</sup> cells  
35 is believed to be attributed to the role of the T4 cell surface glycoprotein as the membrane-anchored virus receptor. Because T4 behaves as the HIV virus

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receptor, its extracellular sequence probably plays a direct role in binding HIV. More specifically, it is believed that HIV envelope selectively binds to the T4 epitope(s), using this interaction to initiate entry into the host cell [A. G. Dalgelish et al., "The CD4 (T4) Antigen Is An Essential Component Of The Receptor For The AIDS Retrovirus", Nature, 312, pp. 763-67 (1984); D. Klatzmann et al., "T-Lymphocyte T4 Molecule Behaves As The Receptor For Human Retrovirus LAV", Nature, 312, pp. 767-68 (1984)]. Accordingly, cellular expression of T4 is believed to be sufficient for HIV binding, with the T4 protein serving as a receptor for the HIV virus.

The T4 tropism of the HIV virus has been demonstrated in vitro. When HIV virus isolated from AIDS patients is cultured together with T helper lymphocytes preselected for surface T4, the lymphocytes are efficiently infected, display cytopathic effects, including multinuclear syncytia formation and are killed by lytic growth [D. Klatzmann et al., "Selective Tropism Of Lymphadenopathy Associated Virus (LAV) For Helper-Inducer T Lymphocytes", Science, 225, pp. 59-63 (1984); F. Wong-Staal and R. C. Gallo, "Human T-Lymphotropic Retroviruses", Nature, 317, pp. 395-403 (1985)]. It has been demonstrated that a cloned cDNA version of human T4, when expressed on the surface of transfected cells from non-T cell lineages, including murine and fibroblastoid cells, endows those cells with the ability to bind HIV [P. J. Maddon et al., "The T4 Gene Encodes The AIDS Virus Receptor And Is Expressed In The Immune System And The Brain", Cell, 47, pp. 333-48 (1986)].

During the course of HIV infection, the host mounts both a humoral and a cellular immune response to the virus. These responses include the appearance of antibodies which bind to a number of viral products and which exhibit neutralizing effect

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or antibody dependent cellular cytotoxic functions [M. Guroff-Robert et al., "HTLV-III-Neutralizing Antibodies In Patients With AIDS And AIDS-Related Complex", Nature, 316, pp. 72-74 (1985); D. D. F. Barin et al., "Virus Envelope Protein Of HTLV-III Represents Major Target Antigen For Antibodies In AIDS Patients", Science, 228, pp. 1094-96 (1985); A. H. Rook et al., "Sera From HTLV-III/LAV Antibody Positive Individuals Mediate Antibody Dependent Cellular Cytotoxicity Against HTLV-III/LAV Infected T Cells", J. Immunol., 138, pp. 1064-68 (1987)]. Epitopes of the HIV envelope have been identified as important determinants in eliciting a neutralizing antibody response. And, determinants in antibody dependent cellular cytotoxicity ("ADCC") activity include HIV env and, possibly, gag epitopes.

In the absence to date of effective treatments for AIDS, many efforts have centered on prevention of the disease. Such preventative measures include HIV antibody screening for all blood, organ and semen donors and education of AIDS high-risk groups regarding transmission of the disease.

Experimental or early-stage clinical treatment of AIDS and ARCS conditions have included the administration of antiviral drugs, such as HPA-23, phosphonoformate, suramin, ribavirin, azidothymidine ("AZT") and dideoxycytidine, which apparently interfere with replication of the virus through reverse transcriptase inhibition. Although each of these drugs exhibits activity against HIV in vitro, only AZT has demonstrated potential benefits in clinical trials. AZT administration in effective amounts, however, has been accompanied by undesirable and debilitating side effects, such as bone marrow depression. It is likely, therefore, that hematologic toxicity will be a major rate limiting factor in the long term use of AZT.

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other proposed methods for treating AIDS have focused on the development of agents having activity against steps in the viral replicative cycle other than reverse transcription. Such methods  
5 include the administration of interferons or the application of hybridoma technology. Most of these treatment strategies are expected to require the co-administration of immunomodulators, such as interleukin-2.

10 To date, the need exists for the development of effective immunotherapeutic agents and methods for the treatment of AIDS, ARCS, HIV infection and other immunodeficiencies caused by T lymphocyte depletion or abnormalities.

15 DISCLOSURE OF THE INVENTION

The present invention solves the problems referred to above by providing, in large amounts, soluble T4 and soluble derivatives thereof that act as receptors for infective agents whose primary target  
20 is the T4 surface protein of T4<sup>+</sup> lymphocytes. Advantageously, this invention also provides soluble T4 essentially free of other proteins of human origin and in a form that is not contaminated by viruses, such as HIV or hepatitis B virus.

25 As will be appreciated from the disclosure to follow, the DNA sequences and recombinant DNA molecules of this invention are capable of directing, in an appropriate host, the production of soluble T4 or derivatives thereof. The polypeptides of this  
30 invention are useful, either as produced in the host or after further derivatization or modification, in a variety of immunotherapeutic compositions and methods for treating immunodeficient patients suffering from diseases caused by infective agents  
35 whose primary targets are T4<sup>+</sup> lymphocytes. According to various embodiments of this invention, such compo-

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sitions and methods relate to a soluble receptor for HIV, soluble T4 proteins and polypeptides and antibodies thereto. The soluble T4 proteins and polypeptides of this invention include monovalent, as well  
5 as polyvalent forms.

The compositions and methods of this invention, which are based upon soluble T4 proteins, polypeptides or peptides and antibodies thereto, are particularly useful for the prevention, treatment or  
10 detection of the HIV-related infections AIDS and ARC. More specifically, the soluble T4-based compositions and methods of this invention employ soluble T4-like polypeptides -- polypeptides which advantageously interfere with the T4/HIV interaction  
15 by blocking or competitive binding mechanisms which inhibit HIV infection of cells expressing the T4 surface protein. These soluble T4-like polypeptides inhibit adhesion between T4<sup>+</sup> lymphocytes and infective agents which target T4<sup>+</sup> lymphocytes and inhibit  
20 interaction between T4<sup>+</sup> lymphocytes and antigen presenting cells and targets of T4<sup>+</sup> lymphocytes mediated killing. By acting as soluble virus receptors, the compositions of this invention may be used as anti-viral therapeutics to inhibit HIV binding to T4<sup>+</sup>  
25 cells and virally induced syncytium formation at the level of receptor binding.

This invention accomplishes these goals by providing DNA sequences coding on expression in an appropriate unicellular host for soluble T4 proteins\*  
30 and soluble derivatives thereof.

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\* As used in this application, "soluble T4 protein", "soluble T4" and "soluble T4-like polypeptides" include all proteins, polypeptides and peptides which  
35 are natural or recombinant soluble T4 proteins, or soluble derivatives thereof, and which are characterized by the immunotherapeutic (anti-retroviral)

(footnote continued on following page)

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This invention also provides recombinant DNA molecules containing those DNA sequences and unicellular hosts transformed with them. Those hosts permit the production of large quantities of the novel soluble T4 proteins, polypeptides, peptides and derivatives of this invention for use in a wide variety of therapeutic, prophylactic and diagnostic compositions and methods

The DNA sequences of this invention are selected from the group consisting of:

- (a) the DNA inserts of p199-7, pBG377, pBG380, pBG381, p203-5, pBG391, pBG392, pBG393, pBG394, pBG395, pBG396, pBG397, p211-11, p214-10 and p215-7;
- (b) DNA sequences which hybridize to one or more of the foregoing DNA inserts and which code on expression for a soluble T4-like polypeptide; and
- (c) DNA sequences which code on expression for a soluble T4-like polypeptide coded for on expression by any of the foregoing DNA inserts and sequences.

According to an alternate embodiment, this invention also relates to a DNA sequence comprising the DNA insert of p170-2, said sequence coding on expression for a T4-like polypeptide. And, this invention also relates to recombinant DNA molecules and processes for producing T4 protein using that DNA sequence.

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(footnote continued from preceding page)

or immunogenic activity of soluble T4 protein. They include soluble T4-like compounds from a variety of sources, such as soluble T4 protein derived from natural sources, recombinant soluble T4 protein and synthetic or semi-synthetic soluble T4 protein.



BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 is an autoradiograph depicting the purification of T4 protein from U937 cells by immunoaffinity chromatography.

Figure 2 depicts autoradiograph and Western blot data demonstrating that immunoaffinity-purified, solubilized native T4 protein binds to HIV envelope protein.

Figure 3 depicts the nucleotide sequence and the derived amino acid sequence of T4 cDNA obtained from PBL clone  $\lambda$ 203-4. In this figure, the amino acids are represented by single letter codes as follows:

Phe: F	Leu: L	Ile: I	Met: M
Val: V	Ser: S	Pro: P	Thr: T
Ala: A	Tyr: Y	His: H	Gln: Q
Asn: N	Lys: K	Asp: D	Glu: E
Cys: C	Trp: W	Arg: R	Gly: G

\* = position at which a stop codon is present.

In Figure 3, the T4 protein translation start (AA<sub>-23</sub>) is located at the methionine at nucleotides 201-203 and the mature N-terminus is located at the lysine (AA<sub>3</sub>) at nucleotides 276-278.

Figure 4 is a schematic outline of the construction of cDNA clones pBG312.T4 (also called p171-1) and p170-2.

Figure 5 is a schematic outline of the construction of plasmid pEC100.

Figure 6 depicts amino acid comparisons at positions 3, 64 and 231 of various T4 cDNA clones.

Figures 7A and 7B depict the protein domain structure of purified, solubilized T4 protein and recombinant soluble T4 mutants.

Figures 8A-8D are schematic outlines of constructions of various intermediate plasmids and other plasmids used to express recombinant soluble T4 ("rst4") of this invention.

Figure 9A is a schematic outline of the construction of plasmid p199-7.

Figures 9B and 9C are schematic outlines of the construction of plasmid p203-5.

5        Figure 10 depicts the synthetic oligo-nucleotide linkers employed in various constructions according to this invention.

10        Figure 11 depicts the nucleotide sequence of the entire plasmid defined by p199-7 ( $P_{Lmutet.rsT4}$ ) and its rsT4.2 insert and the amino acid sequence deduced from the rsT4 sequence. This includes the ClaI-ClaI cassette which defines the Met perfect rsT4.2 coding sequence.

15        Figure 12 depicts a protein blot analysis of an induction of rsT4.2 expression from SG936/p199-7.

Figure 13 is a schematic outline of the construction of plasmid pBG368.

20        Figures 14A-14C are schematic outlines of constructions of various plasmids of this invention.

Figure 15 depicts the nucleotide sequence of plasmid pBG391.

25        Figure 16 depicts the nucleotide sequence of plasmid pBG392. In this figure, the T4 protein translation start (AA<sub>23</sub>) is located at the methionine at nucleotides 1207-1209 and the mature N-terminus is located at the lysine (AA<sub>3</sub>) at nucleotide 1281-84.

30        Figure 17 is a schematic outline of constructions of various plasmids of this invention.

Figure 18 depicts the synthetic oligonucleotide linkers employed in various constructions according to this invention.

35        Figure 19 depicts the nucleotide sequence of plasmid pBG394.

Figure 20 depicts the nucleotide sequence of plasmid pBG396.

Figure 21 depicts the nucleotide sequence of plasmid pBG393.

Figure 22 depicts the nucleotide sequence of plasmid pBG395.

5        Figure 23 is a Coomassie stained gel of rsT4.2 purified from the conditioned medium of the pBG380 transfected CHO cell line BG380G of plasmid p196-10.

10       Figure 24 is a schematic outline of the construction of plasmid p196-10.

Figure 25 is a schematic outline of the construction of plasmid pBG394.

Figure 26 is a schematic outline of the construction of plasmid p211-11.

15       Figure 27 is a schematic outline of the construction of plasmid p215-7.

Figure 28 is a schematic outline of the construction of plasmid p218-8.

20       Figure 29A is a Coomassie stained gel of rsT4.113.1 purified from the conditioned medium of pBG211-11 transfected E.coli.

Figure 29B is an autoradiograph depicting a Western blot analysis of rsT4.113.1 expressed in E.coli.

25       Figure 30, panels (a)-(c) depict the purification of rsT4.113.1 from E.coli transformants.

Figure 31, panels (a)-(c) depict the refolding of purified rsT4.113.1.

30       Figure 32 is an autoradiograph depicting the immunoprecipitation of <sup>35</sup>S-metabolically labelled CHO cell lines producing recombinant soluble T4.

Figure 33 depicts an immunoblot analysis of COS 7 cell lines producing recombinant soluble T4.

35       Figure 34 depicts in graphic form the results of a competition assay between rsT4.113.1 and rsT4.3 for binding to OKT4A or OKT4.

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Figures 35-37 depict in graphic form the results of competition assays between rsT4.111 and rsT4.3 for binding to, respectively, OKT4A, Leu-3A and OKT4.

5 Figure 38 depicts in graphic form an ELISA assay for rsT4.113.1 from E.coli transformants.

Figure 39 depicts in graphic form the results of a p24 radioimmunoassay using recombinant soluble T4 according to this invention.

10 Figures 40 and 41 depict the results of syncytia inhibition assays using recombinant soluble T4 proteins according to this invention.

Figure 42 is a schematic outline of the construction of plasmid pBiv.1.

15 Figure 43 depicts the bivalent recombinant soluble T4 protein produced by pBiv.1.

#### DETAILED DESCRIPTION OF THE INVENTION

We isolated the DNA sequences of this invention from two libraries: a  $\lambda$ gt cDNA library derived the T cell tumor line REX and a  $\lambda$ gt10 cDNA library derived from peripheral blood lymphocytes. However, we could also have employed libraries prepared from other cells that express T4. These include, for example, H9 and U937. We also used a human genomic bank to isolate various fragments of the T4 gene.

For screening these libraries, we used a series of chemically synthesized anti-sense oligonucleotide DNA probes based upon the T4 protein sequence set forth in Maddon et al. (1985), supra.

For screening, we hybridized our oligonucleotide probes to our cDNA libraries utilizing a plaque hybridization screening assay. We selected clones hybridizing to several of our probes. And, after isolating and subcloning the cDNA inserts of the selected clones into plasmids, we determined

their nucleotide sequences and compared the amino acid sequences deduced from those nucleotide sequences to the amino acid sequences referred to in Maddon et al. (1985), supra. As a result of these comparisons, we determined that all of our selected clones were characterized by cDNA inserts coding for amino acid sequences of human T4.

We have depicted in Figure 3 the nucleotide sequence of full-length T4 cDNA obtained from deposited clone p170-2 and the amino acid sequence deduced therefrom. That cDNA sequence was subsequently subjected to in vitro site-directed mutagenesis and restriction fragment substitution so that its cDNA sequence was identical to that of Maddon et al.

After modifying our T4 cDNA sequence to be identical to that of Maddon et al., we truncated samples of it in various positions to remove the coding regions for the transmembrane and intracytoplasmic domains. The remaining cDNA sequences encoded a soluble T4 which retained the extracellular region believed to be responsible for HIV binding.

We then constructed various clones characterized by such cDNA inserts coding for human soluble T4. Those cDNA sequences may be used in a variety of ways in accordance with this invention. More particularly, those sequences or portions of them, or synthetic or semi-synthetic copies of them, may be used as DNA probes to screen other human or animal cDNA or genomic libraries to select by hybridization other DNA sequences that are related to soluble T4. Typically, conventional hybridization conditions, e.g., about 20° to 27°C below T<sub>m</sub>, are employed in such selections. However, less stringent conditions may be necessary when the library is being screened with a probe from a different species than that from

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which the library is derived, e.g., the screening of a mouse library with a human probe.

Such cDNA inserts, portions of them, or synthetic or semi-synthetic copies of them, may also be used as starting materials to prepare various mutations. Such mutations may be either degenerate, i.e., the mutation does not change the amino acid sequence encoded by the mutated codon, or non-degenerate, i.e., the mutation changes the amino acid sequence encoded by the mutated codon. Both types of mutations may be advantageous in producing or using soluble T4's according to this invention. For example, these mutations may permit higher levels of production or easier purification of soluble T4 or higher T4 activity.

For all of these reasons, the DNA sequences of this invention are selected from the group consisting of:

- (a) the DNA inserts of p199-7, pBG377, pBG380, pBG381, p203-5, pBG391, pBG392, pBG393, pBG394, pBG395, pBG396, pBG397, p211-11, p214-10 and p215-7;
- (b) DNA sequences which hybridize to one or more of the foregoing DNA inserts and which code on expression for a soluble T4-like polypeptide; and
- (c) DNA sequences which code on expression for a soluble T4-like polypeptide coded for on expression by any of the foregoing DNA inserts and sequences.

Preferably, the DNA sequences of this invention code for a polypeptide selected from the group consisting of a polypeptide of the formula AA<sub>23</sub>-AA<sub>362</sub> of Figure 3, a polypeptide of the formula AA<sub>1</sub>-362 of Figure 3, a polypeptide of the formula Met-AA<sub>1</sub>-362 of Figure 3, a polypeptide of the formula AA<sub>1</sub>-374 of Figure 3, a polypeptide of the formula Met-AA<sub>1</sub>-374 of Figure 3, a polypeptide of the formula AA<sub>1</sub>-377 of Figure 3, a polypeptide of the formula

Met-AA<sub>1-377</sub> of Figure 3, a polypeptide of the formula  
AA<sub>-23-AA<sub>374</sub></sub> of Figure 3, a polypeptide of the formula  
AA<sub>-23-AA<sub>377</sub></sub> of Figure 3, or portions thereof.

DNA sequences according to this invention  
5 also preferably code for a polypeptide selected from  
the group consisting of a polypeptide of the formula  
AA<sub>-23-AA<sub>182</sub></sub> of Figure 16, a polypeptide of the  
formula AA<sub>1-AA<sub>182</sub></sub> of Figure 16, a polypeptide of  
the formula Met-AA<sub>1-182</sub> of Figure 16, a polypeptide  
10 of the formula AA<sub>-23-AA<sub>182</sub></sub> of Figure 16, followed by  
the amino acids asparagine-leucine-glutamine-histidine-  
serine-leucine, a polypeptide of the formula  
AA<sub>1-AA<sub>182</sub></sub> of Figure 16, followed by the amino acids  
asparagine-leucine-glutamine-histidine-serine-leucine,  
15 a polypeptide of the formula Met-AA<sub>1-182</sub> of Figure 16,  
followed by the amino acids asparagine-leucine-  
glutamine-histidine-serine-leucine, a polypeptide of  
the formula AA<sub>-23-AA<sub>113</sub></sub> of Figure 16, a polypeptide  
of the formula AA<sub>1-AA<sub>113</sub></sub> of Figure 16, a polypeptide  
20 of the formula Met-AA<sub>1-113</sub> of Figure 16, a polypeptide  
of the formula AA<sub>-23-AA<sub>111</sub></sub> of Figure 16, a polypeptide  
of the formula AA<sub>1-AA<sub>111</sub></sub> of Figure 16, a polypeptide  
of the formula Met-AA<sub>1-111</sub> of Figure 16, a polypep-  
tide of the formula AA<sub>-23-AA<sub>131</sub></sub> of Figure 16, a poly-  
25 peptide of the formula AA<sub>1-AA<sub>131</sub></sub> of Figure 16, a  
polypeptide of the formula Met-AA<sub>1-131</sub> of Figure 16,  
a polypeptide of the formula AA<sub>-23-AA<sub>145</sub></sub> of Figure 16,  
a polypeptide of the formula AA<sub>1-AA<sub>145</sub></sub> of Figure 16,  
a polypeptide of the formula Met-AA<sub>1-145</sub> of Figure 16,  
30 a polypeptide of the formula AA<sub>-23-AA<sub>166</sub></sub> of Figure 16,  
a polypeptide of the formula AA<sub>1-AA<sub>166</sub></sub> of Figure 16,  
a polypeptide of the formula Met-AA<sub>1-166</sub> of Figure 16,  
or portions thereof.

Additionally, DNA sequences of this inven-  
35 tion code for a polypeptide selected from the group  
consisting of a polypeptide of the formula AA<sub>-23-AA<sub>362</sub></sub>  
of mature T4 protein, a polypeptide of the formula  
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AA<sub>1-362</sub> of mature T4 protein, a polypeptide of the formula Met-AA<sub>1-362</sub> of mature T4 protein, a polypeptide of the formula AA<sub>1-374</sub> of mature T4 protein, a polypeptide of the formula Met-AA<sub>1-374</sub> of mature T4 protein, a polypeptide of the formula AA<sub>1-377</sub> of mature T4 protein, a polypeptide of the formula Met-AA<sub>1-377</sub> of mature T4 protein, a polypeptide of the formula AA<sub>23-AA374</sub> of mature T4 protein, a polypeptide of the formula AA<sub>23-AA377</sub> of mature T4 protein, or portions thereof.

DNA sequences according to this invention also code for a polypeptide selected from the group consisting of a polypeptide of the formula AA<sub>23-AA182</sub> of mature T4 protein, a polypeptide of the formula AA<sub>1-AA182</sub> of mature T4 protein, a polypeptide of the formula Met-AA<sub>1-182</sub> of mature T4 protein, a polypeptide of the formula AA<sub>23-AA182</sub> of mature T4 protein, followed by the amino acids asparagine-leucine-glutamine-histidine-serine-leucine, a polypeptide of the formula AA<sub>1-AA182</sub> of mature T4 protein, followed by the amino acids asparagine-leucine-glutamine-histidine-serine-leucine, a polypeptide of the formula Met-AA<sub>1-182</sub> of mature T4 protein, followed by the amino acids asparagine-leucine-glutamine-histidine-serine-leucine, a polypeptide of the formula AA<sub>23-AA113</sub> of mature T4 protein, a polypeptide of the formula AA<sub>1-AA113</sub> of mature T4 protein, a polypeptide of the formula Met-AA<sub>1-113</sub> of mature T4 protein, a polypeptide of the formula AA<sub>23-AA111</sub> of mature T4 protein, a polypeptide of the formula AA<sub>1-AA111</sub> of mature T4 protein, a polypeptide of the formula Met-AA<sub>1-111</sub> of mature T4 protein, a polypeptide of the formula AA<sub>23-AA131</sub> of mature T4 protein, a polypeptide of the formula AA<sub>1-AA131</sub> of mature T4 protein, a polypeptide of the formula Met-AA<sub>1-131</sub> of mature T4 protein, a polypeptide of the formula AA<sub>23-AA145</sub> of mature T4 protein, a polypeptide of

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the formula  $AA_1-AA_{145}$  of mature T4 protein, a polypeptide of the formula  $Met-AA_{1-145}$  of mature T4 protein, a polypeptide of the formula  $AA_{23}-AA_{166}$  of mature T4 protein, a polypeptide of the formula  $AA_1-AA_{166}$  of mature T4 protein, a polypeptide of the formula  $Met-AA_{1-166}$  of mature T4 protein, or portions thereof.

The amino terminal amino acid of mature T4 protein isolated from T cells begins at lysine, the third amino acid of the sequence depicted in Figure 16. Accordingly, soluble T4 proteins also include polypeptides of the formula  $AA_3-AA_{377}$  of Figure 16, or portions thereof. Such polypeptides include polypeptides selected from the group consisting of a polypeptide of the formula  $AA_3$  to  $AA_{362}$  of Figure 16, a polypeptide of the formula  $AA_3$  to  $AA_{374}$  of Figure 16, a polypeptide of the formula  $AA_3-AA_{182}$  of Figure 16, a polypeptide of the formula  $AA_3-AA_{113}$  of Figure 16, a polypeptide of the formula  $AA_3-AA_{131}$  of Figure 16, a polypeptide of the formula  $AA_3-AA_{145}$  of Figure 16, a polypeptide of the formula  $AA_3-AA_{166}$  of Figure 16, and a polypeptide of the formula  $AA_3-AA_{111}$  of Figure 16. Soluble T4 proteins also include the above-recited polypeptides preceded by an N-terminal methionine group.

Soluble T4 protein constructs according to this invention may also be produced by truncating the full length T4 protein sequence at various positions to remove the coding regions for the transmembrane and intracytoplasmic domains, while retaining the extracellular region believed to be responsible for HIV binding. More particularly, soluble T4 polypeptides may be produced by conventional techniques of oligonucleotide directed mutagenesis; restriction digestion, followed by insertion of linkers; or chewing back full length T4 protein with enzymes.

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Alternatively, soluble T4 polypeptides may be chemically synthesized by conventional peptide synthesis techniques, such as solid phase synthesis [R. B. Merrifield, "Solid Phase Peptide Synthesis. I. The Synthesis Of A Tetrapeptide", J. Am. Chem. Soc., 83, pp. 2149-54 (1963)].

The DNA sequences of this invention code for soluble proteins and derivatives that are believed to bind to Major Histocompatibility Complex antigens and envelope glycoprotein of certain retroviruses, such as HIV. Preferably, they also inhibit syncytium formation, believed to be the mode of intracellular HIV virus spread. And, they may inhibit interaction between T4<sup>+</sup> lymphocytes and antigen-presenting cells and targets of T4<sup>+</sup> cell mediated killing. Most preferably, they also inhibit adhesion between T4<sup>+</sup> lymphocytes and infective agents, such as the HIV virus, whose primary targets are T4<sup>+</sup> lymphocytes.

The DNA sequences of this invention are also useful for producing soluble T4 or its derivatives coded for on expression by them in unicellular hosts transformed with those DNA sequences. As well known in the art, for expression of the DNA sequences of this invention, the DNA sequence should be operatively linked to an expression control sequence in an appropriate expression vector and employed in that expression vector to transform an appropriate unicellular host.

Such operative linking of a DNA sequence of this invention to an expression control sequence, of course, includes the provision of a translation start signal in the correct reading frame upstream of the DNA sequence. If the particular DNA sequence of this invention being expressed does not begin with a methionine, the start signal will result in an additional amino acid -- methionine -- being located at the N-terminus of the product. While

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such methionyl-containing product may be employed directly in the compositions and methods of this invention, it is usually more desirable to remove the methionine before use. Methods are available in the art to remove such N-terminal methionines from polypeptides expressed with them. For example, certain hosts and fermentation conditions permit removal of substantially all of the N-terminal methionine in vivo. Other hosts require in vitro removal of the N-terminal methionine. However, such in vivo and in vitro methods are well known in the art.

A wide variety of host/expression vector combinations may be employed in expressing the DNA sequences of this invention. Useful expression vectors, for example, may consist of segments of chromosomal, non-chromosomal and synthetic DNA sequences, such as various known derivatives of SV40 and known bacterial plasmids, e.g., plasmids from E.coli including col E1, pCR1, pBR322, pMB9 and their derivatives, wider host range plasmids, e.g., RP4, phage DNAs, e.g., the numerous derivatives of phage  $\lambda$ , e.g., NM989, and other DNA phages, e.g., M13 and filamentous single stranded DNA phages, yeast plasmids, such as the 2 $\mu$  plasmid or derivatives thereof, and vectors derived from combinations of plasmids and phage DNAs, such as plasmids which have been modified to employ phage DNA or other expression control sequences. For animal cell expression, we prefer to use plasmid pBG368, a derivative of pBG312 [R. Cate et al., "Isolation Of The Bovine And Human Genes For Mullerian Inhibiting Substance And Expression Of The Human Gene In Animal Cells", Cell, 45, pp. 685-98 (1986)] which contains the major late promoter of adenovirus 2.

In addition, any of a wide variety of expression control sequences -- sequences that con-

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trol the expression of a DNA sequence when operatively linked to it -- may be used in these vectors to express the DNA sequence of this invention. Such useful expression control sequences, include, for example, the early and late promoters of SV40 or the adenovirus, the lac system, the trp system, the TAC or TRC system, the major operator and promoter regions of phage  $\lambda$ , the control regions of fd coat protein, the promoter for 3-phosphoglycerate kinase or other glycolytic enzymes, the promoters of acid phosphatase, e.g., Pho5, the promoters of the yeast  $\alpha$ -mating factors, the polyhedron promoter of the baculovirus system and other sequences known to control the expression of genes of prokaryotic or eukaryotic cells or their viruses, and various combinations thereof. For animal cell expression, we prefer to use an expression control sequence derived from the major late promoter of adenovirus 2.

A wide variety of unicellular host cells are also useful in expressing the DNA sequences of this invention. These hosts may include well known eukaryotic and prokaryotic hosts, such as strains of E.coli, Pseudomonas, Bacillus, Streptomyces, fungi, such as yeasts, and animal cells, such as CHO and mouse cells, African green monkey cells, such as COS 1, COS 7, BSC 1, BSC 40, and BMT 10, insect cells, and human cells and plant cells in tissue culture. For animal cell expression, we prefer CHO cells and COS 7 cells.

It should of course be understood that not all vectors and expression control sequences will function equally well to express the DNA sequences of this invention. Neither will all hosts function equally well with the same expression system. However, one of skill in the art may make a selection among these vectors, expression control sequences, and hosts without undue experimentation and without

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departing from the scope of this invention. For example, in selecting a vector, the host must be considered because the vector must replicate in it. The vector's copy number, the ability to control that copy number, and the expression of any other proteins encoded by the vector, such as antibiotic markers, should also be considered.

In selecting an expression control sequence, a variety of factors should also be considered. These include, for example, the relative strength of the system, its controllability, and its compatibility with the particular DNA sequence of this invention, particularly as regards potential secondary structures. Unicellular hosts should be selected by consideration of their compatibility with the chosen vector, the toxicity of the product coded for on expression by the DNA sequences of this invention to them, their secretion characteristics, their ability to fold proteins correctly, their fermentation requirements, and the ease of purification of the products coded on expression by the DNA sequences of this invention.

Within these parameters, one of skill in the art may select various vector/expression control system/host combinations that will express the DNA sequences of this invention on fermentation or in large scale animal culture, e.g., CHO cells or COS 7 cells.

The polypeptides produced on expression of the DNA sequences of this invention may be isolated from the fermentation or animal cell cultures and purified using any of a variety of conventional methods. One of skill in the art may select the most appropriate isolation and purification techniques without departing from the scope of this invention.

The polypeptides produced on expression of the DNA sequences of this invention are essentially

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free of other proteins of human origin. Thus, they are different than T4 protein purified from human lymphocytes.

The polypeptides of this invention are useful in immunotherapeutic compositions and methods. For example, the polypeptides of this invention are active in inhibiting infection by agents whose primary targets are T4<sup>+</sup> lymphocytes by interfering with their interaction with those target lymphocytes. More preferably, the polypeptides of this invention may be employed to saturate the T4 receptor sites of T4-targeted infective agents. Thus, they exert anti-viral activity by competitive binding with cell surface T4 receptor sites. This effect is plainly of great utility in diseases, such as AIDS, ARC and HIV infection. Accordingly, the polypeptides and methods of this invention may be used to treat humans having AIDS, ARC, HIV infection or antibodies to HIV. In addition, these polypeptides and methods may be used for treating AIDS-like diseases caused by retroviruses, such as simian immunodeficiency viruses, in mammals, including humans.

According to one embodiment of this invention, antibodies to soluble T4 proteins and polypeptides may be used in the treatment, prevention, or diagnosis of AIDS, ARC and HIV infection.

The polypeptides of this invention may also be used in combination with other therapeutics used in the treatment of AIDS, ARC and HIV infection. For example, soluble T4 polypeptides may be used in combination with anti-retroviral agents that block reverse transcriptase, such as AZT, HPA-23, phosphonoformate, suramin, ribavirin and dideoxycytidine. Additionally, these polypeptides may be used with anti-viral agents such as interferons, including alpha interferon, beta interferon and gamma interferon, or glucosidase inhibitors, such as

castanospermine. Such combination therapies advantageously utilize lower dosages of those agents, thus avoiding possible toxicity.

And, the polypeptides of this invention  
5 may be used in plasmapheresis techniques or in blood bags for selective removal of viral contaminants from blood. According to this embodiment of the invention, soluble T4 polypeptides may be coupled to  
10 a solid support, comprising, for example, plastic or glass beads, or a filter, which is incorporated into a plasmapheresis unit.

Additionally, the compositions of this invention may be employed as immunosuppressants useful in preventing or treating graft-vs-host disease,  
15 autoimmune diseases and allograft rejection.

The compositions of this invention typically comprise an immunotherapeutic effective amount of a polypeptide of this invention and a pharmaceutically acceptable carrier. Therapeutic methods of  
20 this invention comprise the step of treating patients in a pharmaceutically acceptable manner with those compositions.

The compositions of this invention for use in these therapies may be in a variety of forms.  
25 These include, for example, solid, semi-solid and liquid dosage forms, such as tablets, pills, powders, liquid solutions or suspensions, liposomes, suppositories, injectable and infusable solutions. The preferred form depends on the intended mode of administration and therapeutic application. The compositions  
30 also preferably include conventional pharmaceutically acceptable carriers and adjuvants which are known to those of skill in the art.

Generally, the pharmaceutical compositions  
35 of the present invention may be formulated and administered using methods and compositions similar to those used for other pharmaceutically important poly-

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peptides (e.g., alpha-interferon). Thus, the polypeptides may be stored in lyophilized form, reconstituted with sterile water just prior to administration, and administered by the usual routes of administration such as parenteral, subcutaneous, intravenous, intramuscular or intralesional routes. An effective dosage may be in the range of from 0.5 to 5.0 mg/kg body weight/day, it being recognized that lower and higher doses may also be useful.

This invention also relates to soluble receptors and their use in diagnosing or treating viral agents which target or bind to those receptors. Such soluble receptors may be used as decoys to absorb viral agents and to halt the spread of viral infection. Alternatively, virus-killing agents may be attached to the soluble protein receptors, providing a direct mode of delivery of those agents to the virus.

More particularly, the polypeptides of this invention are useful in diagnostic compositions and methods to detect or monitor the course of HIV infection. Advantageously, these polypeptides are useful in diagnosing variants of the HIV virus, regardless of origin of the infecting HIV agent.

For example, soluble T4 proteins and polypeptides according to this invention, which have a high affinity for HIV, may be advantageously used to increase the sensitivity of HIV assay systems now based upon monoclonal or polyclonal antibodies.

More specifically, soluble T4 proteins and polypeptides may be used to pretreat test plasma to concentrate any HIV present, even in small amounts, so that it is more easily recognized by the antibody. And soluble T4 proteins and polypeptides may be used to purify the HIV envelope protein gp120.

Alternatively, the soluble T4 proteins and polypeptides of this invention may be used to replace

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anti-HIV antibodies now used in various assays. These soluble T4 proteins and polypeptides are preferable to anti-HIV antibodies for two reasons. First, soluble T4, exhibits an affinity for HIV of approximately  $10^{-9}$ , a level which exceeds the  $10^{-7}$  to  $10^{-8}$  values of anti-HIV antibodies. And, while anti-HIV antibodies are more likely to be specific for different HIV isolates, strain variations would not affect a soluble T4 protein-based assay, since all HIV isolates must be capable of interacting with the T4 receptor as a prerequisite to infectivity.

For example, a soluble T4 protein or polypeptide may be linked to an indicator, such as an enzyme, and used in an ELISA assay. Here, soluble T4 advantageously acts as a measure of both HIV in a test sample and any free HIV envelope gp120 protein.

And, polyvalent forms of soluble T4 proteins or polypeptides may be produced, for example, by chemical coupling or genetic fusion techniques, thus increasing even further the avidity of soluble T4 for HIV.

In order that this invention may be better understood, the following examples are set forth. These examples are for purposes of illustration only, and are not to be construed as limiting the scope of the invention in any manner.

#### EXAMPLES

##### Purification Of Native Solubilized T4

We purified native T4 from the T4<sup>+</sup>-promonocytic cell line U937 derived from a histocytic lymphoma to approximately 50% purity using immunoaffinity chromatography as follows.

We grew U937 cells [a gift from Dr. Scott Hammer, New England Deaconess Hospital] to  $10^6$  cells/ml in RPMI 1640, 10% FCS, harvested and washed them in 1X PBS. We then lysed the cell pellet

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in 20 mM Tris-HCl (pH 7.7), 0.5% NP-40 (a non-ionic detergent), 0.2% NaDOC, 0.2 mM EGTA, 0.2 mM PMSF and 5 µg/ml BPTI at  $4 \times 10^7$  cells/ml. Because this purification was carried out in the presence of a non-ionic detergent, T4, which is normally membrane-bound via its hydrophobic transmembrane domain, was isolated as a solubilized protein. We spun the lysate in a GS 3 rotor for 10 min at 10,000 rpm and stored the supernatant at -70°C.

Subsequently, we preabsorbed the clarified cell extract with mouse IgG-Sepharose, followed by protein A Sepharose and then passed the flowthrough through an immunoaffinity column comprising immobilized 19Thy anti-T4 monoclonal antibody on Affigel-10 [a gift from Dr. Ellis Reinherz, Dana Farber Cancer Institute, Boston, Massachusetts]. We washed the column extensively and eluted the bound material with 50 mM glycine-HCl (pH 2.5), 0.15 M NaCl, 0.5% NP-40, 5 µg/ml BPTI and 0.2 mM EGTA.

We then separated 10 µl aliquots of each elution fraction on a 10% SDS-PAGE under reducing conditions, with the bands being visualized by silver staining. As shown in Figure 1, a major silver-stained band of 55 Kd was visible. We then carried out two assays on the 55 Kd protein and sequenced the amino terminus of the protein to confirm its identity as native solubilized T4.

#### Sequencing Of Native Solubilized T4

We determined the N-terminal amino acid sequence of our solubilized native T4 which we isolated from a detergent extract of U937 cells by immunoaffinity chromatography as described above.

Techniques for determining the amino acid sequences of various proteins and peptides derived from them are well known in the art. We chose automated Edman degradation to determine the amino

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terminus of our solubilized native T4. More specifically, we gel purified and electrophoretically separated approximately 5 µg of the solubilized native T4 and then subjected it to automated Edman degradation using a gas phase sequencer (Applied Biosystems 470A). We then identified the PTH-amino acids produced at each cycle of the Edman chemistry by high pressure liquid chromatography, on-line with the sequencer, in a PTH-amino acid analyzer (Applied Biosystems 120A). Direct analysis of the protein provided amino terminal sequence information which, when compared to the amino acid sequence deduced from the cDNA sequence of human T4 [Maddon et al. (1985), supra], identified the purified protein as human T4.

#### 15 Radioimmunoassay Of Native Solubilized T4

To determine that our purification process enriched for T4, we assayed fractions from the immunoaffinity elution step in a T4-specific sandwich radioimmunoassay, based upon the ELISA assay of P. E. Rao et al., in Cellular Immunology, 80, pp. 310-19 (1983). We coated each well of a Removawell strip (Dynatech Labs, Alexandria, Virginia) with 50 µl of 10 µl/ml OKT4 antibody (ATCC #CRL 8002) or MOPC195 (a background binding control) in 0.05 M sodium bicarbonate buffer (pH 9.4) at 4°C overnight. We washed the wells and then filled them with 1% FCS in PBS to saturate the protein binding capacity of the plastic. After removing the 1% FCS solution, we added test samples, in 50 µl aliquots, to the wells. We then incubated the samples for 4 hours at room temperature. Subsequently, we removed the samples and washed the wells four times with 0.05% Tween-20 in PBS. We then added <sup>125</sup>I-labelled 19Thy antibody (50,000-100,000 cpm per well) and incubated the wells at 4°C overnight. We then washed the wells four

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times and separated each well for bound  $^{125}\text{I}$  detection in a Beckman gamma detector.

As shown in Figure 1, in which values were plotted following subtraction for background, the peak fraction of solubilized native T4 protein detected by radioimmunoassay coincided with elution of the 55 Kd protein seen by silver staining.

#### Western Blot Assay For T4

Although many antibodies have been developed for detecting T4 antigen, none are useful for protein blot analysis (Dr. Ellis Reinherz, personal communication). In order to develop antibodies useful for Western blot detection of soluble T4 to follow the purification of T4 and recombinant soluble T4, we raised polyclonal, hyperimmune anti-T4 antisera in rabbits against three synthetic T4 oligopeptides. These oligopeptides are represented in Figure 3 as follows:

	<u>Oligopeptide</u>	<u>Amino Acid Coordinates</u>
20	JB-1	44-63
	JB-2	133-156
	JB-3	325-343

We had previously synthesized these peptides using conventional phosphoamide DNA synthesis techniques. See, e.g., Tetrahedron Letters, 22, pp. 1859-62 (1981). We synthesized the peptides on an Applied Biosystems 380A DNA Synthesizer and purified them by gel electrophoresis.

#### (i) Coupling Of T4 Peptides To BTG

We coupled each of these peptides to the carrier protein bovine thyroglobulin ("BTG") [Sigma, St. Louis, Missouri] according to a modification of procedures set forth in J. Rothbard et al., J. Exp. Med., 160, pp. 208-21 (1984) and R. C. Kennedy et al., "Antiserum To A Synthetic Peptide Recognizes The

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HTLV-III Envelope Glycoprotein", Science, 231, pp. 1556-59 (1986).

More specifically, we mixed 10 mg of BTG diluted in 1 ml of PBS with 1.3 mg of m-maleimido-benzoyl-N-hydroxysuccinimide ester ("MBS") in 0.5 ml of dimethylformamide ("DMF"). We mixed the reaction mixture well and reacted it for about 1 hour at 25°C. Subsequently, we loaded the mixture onto a Sephadex G25 gel filtration column (Pharmacia, Sweden) which had been pre-equilibrated with 0.1 M PBS (pH 6.0). We then collected a total of thirty 2 ml aliquot elution fractions and read the absorbance of each fraction at 280 nm (" $A_{280}$ "). We then pooled the three peak fractions (15, 16 and 17) to create the activated carrier.

We dissolved 10 mg of  $\text{NaBH}_4$  in 2.5 ml of 0.1 M sodium borate solution to produce a sodium borohydride solution. Subsequently, we diluted approximately 8 mg of each of synthetic T4 peptides JB-1, JB-2 and JB-3 with 1 ml of 0.1 M borate buffer and then mixed each solution with 200  $\mu\text{l}$  of the sodium borohydride solution, incubating the mixture on ice for 5 minutes. We then warmed each peptide solution to 25°C, brought each solution to pH 1.0 with 1 N HCl (during which frothing occurred) and then brought each solution to pH 7.0 with 1 N NaOH (after the frothing had stopped).

We then coupled each peptide to BTG by adding 1.2 ml of the peptide solution to 6 ml of the activated carrier solution. We allowed the coupling reaction to proceed overnight by incubating the reaction mixture at room temperature.

#### (ii) Inoculation Of Test Animals

We dissolved each of the BTG-coupled peptides prepared above in sterile Freund's complete adjuvant, to a final concentration of 1  $\mu\text{g}/\text{ml}$  coupled

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peptide in PBS. Subsequently, we inoculated each of three rabbits (New Zealand white) by intramuscular injection of 500 µg of one of the coupled peptides into each rabbit. We inoculated a fourth rabbit (New Zealand white) in the same manner with a mixture of the three coupled peptides. All rabbits were prebled prior to boosting to establish an average baseline for each response to be measured. The rabbits were boosted at 6 weeks with 500 µg coupled peptide in incomplete Freund's adjuvant.

Serum was collected from each rabbit monthly for 4 months after immunization. The serum was then assayed for anti-peptide titer.

(iii) ELISA With Anti-peptide Sera Against Peptide Coated Plates

In this assay, we determined that antiserum raised in an animal by each of peptides JB-1, JB-2 and JB-3 binds to that peptide. Accordingly, those peptides are immunogenic and elicit a response in test animals.

To carry out the assay, we coated Immulon-2 (Dynatech Labs, Alexandria, Virginia) microtiter plates with 50 µl per well of 50 µg/ml uncoupled peptide in PBS and incubated the plates overnight at 4°C. Plates coated with peptide 46R\*, which served as controls, were treated identically. We then washed the plates 4 times with PBS-Tween (0.5%) and 4 times with water. The plates were blotted dry by gentle tapping over paper towels. After blotting the plates,

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\* Peptide 46 corresponds to amino acids ("AA") 728-751 of the env gene of the HIV genome. The amino acid numbering corresponds to that set forth for the env gene in L. Ratner et al., "Complete Nucleotide Sequence Of The AIDS Virus, HTLV-III", Nature, 313, pp. 277-84 (1985). Peptide 46 has the sequence:

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LPIPRGPD RPEGIEEEGGERDRDR.

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we added 200  $\mu$ l of a 5% FCS/PBS solution to each well and incubated the plates for 1 hour at room temperature.

We then assayed serum samples from the rabbits on the pre-coated plates prepared as described above. We assayed the antibody response to the immunogen peptide at an initial dilution of 1:100, followed by serial 10-fold dilutions in 5% FCS/PBS.

After a 2 hour incubation period at room temperature, we washed the plates and blotted them dry as described above. We then added 50  $\mu$ l of a 1:1500 dilution of horseradish peroxidase ("HRP")-conjugated goat anti-rabbit-IgG [Cooper Biomedical, Malvern, Pennsylvania] in 5% FCS/PBS to each well and incubated the plates at room temperature for 1 hour. We washed the plates with PBS-Tween 0.5%. We then added 50  $\mu$ l of 0.42 mM TMB. We stopped the enzyme reactions with 50  $\mu$ l of 2 M  $H_2SO_4$ . We then analyzed the plates spectrophotometrically at 450 nm using a microtiter plate reader [Dynatech Labs, Alexandria, Virginia].

We observed that antiserum against each of peptides JB-1, JB-2 and JB-3 binds to the corresponding peptide. We also observed that antiserum against a mixture of peptides JB-1, JB-2 and JB-3 binds to peptides JB-1 and JB-3 under the conditions set forth above. The titers of each of the four antisera tested against the peptides in the solid-phase ELISA are shown below, where "ND" represents values not determined:

Peptide	Approximate Titer Against:		
	JB-1	JB-2	JB-3
JB-1	>1/50,000	0	ND
JB-2	0	1/50,000	ND
JB-3	0	0	1/10,000
JB-1 + JB-2 + JB-3	1/4,000	ND	1/7,000

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Ig fractions from two of the three anti-peptide sera raised against individual peptides, anti-JB-1 and anti-JB-2, recognized the 55 Kd T4 antigen band of native solubilized T4 in a Western blot analysis of protein eluted from the 19Thy (anti-T4) monoclonal antibody affinity column described above. As in the case of the radioimmunoassay of native solubilized T4, the detection of the 55 Kd protein coincides with its apparent elution from the affinity column. This provides further evidence that our T4 purification procedure enriched for solubilized T4.

Thus, these polyclonal sera are useful in the detection of nanogram quantities of T4 (both native and recombinant forms) by Western analysis.

#### Binding of Cell-Free T4 To HIV Envelope

We then tested our purified solubilized native T4 isolated from U937 cells for its ability to bind to the HIV envelope protein gp160/gp120. To carry out this direct binding assay, we incubated <sup>35</sup>S-labelled gp160/gp120 detergent cell extract derived from a recombinant cell line 7d2 (a gift from Drs. Mark Kowalski and William Haseltine, Dana-Farber Cancer Institute) with samples of solubilized native T4, each of which had been preincubated with one type of monoclonal antibody.

More specifically, we mixed 5 µl of solubilized T4 in a microfuge tube with 5 µg (about 3 µl) of OKT4 (ATCC #CRL 8002), a monoclonal antibody recognizing an epitope on T4 which does not interfere with HIV binding [J. A. Hoxie et al., J. Immunol., 136, pp. 361-63 (1986)] or with 5 µg of OKT4A (Ortho Diagnostics #7142), a monoclonal antibody that interferes with HIV binding to T4 positive cells [J. Steven McDougal et al., J. Immunol., 137, pp. 2937-2944 (1986)]. Alternatively, we mixed 50 µl of solubilized



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T4 with 5 µg of αHTLV III gp120 (Dupont #NEN-9284). We then incubated the mixtures on ice for 1 hour.

Subsequently, we added 150 µl of <sup>35</sup>S-labelled gp160/gp120 cell extract or <sup>35</sup>S-labelled control cell extract (precleared with protein-A Sepharose) to the preincubated solubilized T4/monoclonal antibody mixtures and rocked the tubes overnight at 4°C. We then precipitated the T4/gp160/gp120 immune complexes by adding 30 µl of protein-A Sepharose to each tube and rocking for 2 hours at 4°C to allow the protein-A Sepharose to bind to the antibody complexes. Subsequently, we spun down the beads in an Eppendorf microfuge and after extensive washings, we eluted with 40 µl SDS sample buffer at 65°C for 10 minutes. We then loaded 20 µl of the eluted material on a 7.5% SDS-PAGE gel which was run under reducing conditions.

Figure 2 depicts autoradiograph and Western blot results of the T4/gp160/gp120 coimmunoprecipitations. In Figure 2, lanes 1-5 were autoradiographed after treatment with 40% sodium salicylate and lanes 6-7 were developed on a Western blot with rabbit antisera JB-2.

As shown in Figure 2, gp160/gp120 protein was coimmunoprecipitated in the presence of T4 with OKT4 (lane 5) but not in the presence of T4 with OKT4A (lane 4). Lane 3 shows the positive control for gp160/gp120 using αHTLV III gp120 monoclonal antibody. Neither negative control with <sup>35</sup>S-labelled control extract (lane 1) or protein-A Sepharose alone (lane 2) showed bands migrating in the position of gp160/gp120. Based upon the bands that developed on the Western blot, the amount of T4 precipitated with either OKT4 (lane 6) or OKT4A (lane 7) appeared to be similar.

This demonstrates that purified, solubilized native T4, which is naturally membrane bound, can

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still interact with the HIV glycoprotein in solution. Accordingly, we believe that cell free soluble T4 is useful in preventing the binding interaction between HIV and the T4 receptor of T4<sup>+</sup> lymphocytes. By competing with cell surface T4 for binding to the HIV envelope protein gp120, soluble T4 is useful in blocking HIV infection.

#### Synthesis Of Oligonucleotide DNA Probes

The nucleotide sequence and a deduced amino acid sequence for a cDNA that purportedly encodes the entire human T4 protein have been reported [Maddon et al., (1985), supra]. The deduced primary structure of the T4 protein reveals that it can be divided into domains as demonstrated below:

15	<u>Structure/Proposed Location</u>	<u>Amino Acid Coordinates</u>
	Hydrophobic/Secretory Signal	-23 to -1
	Homology to V-Regions/ Extracellular	+1 to +94
20	Homology to J-Regions/ Extracellular	+95 to +109
	Glycosylated Region/ Extracellular	+110 to +374
25	Hydrophobic/Transmembrane Sequence	+375 to +395
	Very Hydrophilic/ Intracytoplasmic	+396 to +435

Based on the sequence for the above-listed domains, we chemically synthesized antisense oligonucleotide DNA probes using conventional phosphoamide DNA synthesis techniques. See, e.g., Tetrahedron Letters, 22, pp. 1859-62 (1981). We synthesized the probes on an Applied Biosystems 380A DNA synthesizer and purified them by gel electrophoresis.

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Furthermore, we synthesized the probes such that they were complementary to the DNA sequences which code for the amino acid sequence, i.e., the probes were antisense, to enable them to recognize and hybridize to the corresponding sequences in DNA, as well as in mRNA. The nucleotide sequences of the eleven selected regions of the T4 protein [corresponding to the nucleotide numbering set forth in Maddon et al., (1985), *supra*] were the following:

	<u>Oligonucleotide</u>	<u>Nucleotide Coordinates</u>
10	1	145-171
	2	742-765
	3	1414-1440
15	6	427-453
	7	1303-1329
	8	1012-1038
	9	97-118
	10	10-36
20	11	1698-1724
	12	397-423
	14	261-287

Before using our DNA probes for screening, we 5' end-labelled each of the single-stranded DNA probes with  $^{32}\text{P}$  using  $[\gamma\text{-}^{32}\text{P}]\text{-ATP}$  and T4 polynucleotide kinase, substantially as described by A. M. Maxam and W. Gilbert, "A New Method For Sequencing DNA", Proc. Natl. Acad. Sci. USA, 74, pp. 560-64 (1977).

#### 30 Construction of $\lambda$ gt10 Peripheral Blood Lymphocytes cDNA Library

To prepare our Peripheral Blood Lymphocytes (PBL) cDNA library, we processed PBL, from a single leukophoresis donor, through one round of absorption

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to remove monocytes. We then stimulated the non-adherent cells with IFN- $\gamma$  1000  $\mu$ /ml and 10  $\mu$ g/ml PHA for 24 hours. We isolated RNA from these cells using phenol extraction [Maniatis et al., Molecular Cloning, p. 187 (Cold Spring Harbor Laboratory) (1982)] and prepared poly A<sup>+</sup> mRNA by one round of oligo dT cellulose chromatography. We ethanol precipitated the RNA, dried it in a speed vac and resuspended the RNA in 10  $\mu$ l H<sub>2</sub>O (0.5  $\mu$ g/ $\mu$ l). We treated the RNA for 10 min at room temperature in CH<sub>3</sub>FgOH (5 mM final concentration) and  $\beta$ -mercaptoethanol (0.26 M). We then added the methyl mercury treated RNA to 0.1 M Tris-HCl (pH 8.3) at 43°C, 0.01 M Mg, 0.01 M DTT, 2 mM Vanadyl complex, 5  $\mu$ g oligo dT<sub>12-18</sub>, 20 mM KCl, 1 mM dCTP, dGTP, dTTP, 0.5 mM dATP, 2  $\mu$ Ci[ $\alpha$ -<sup>32</sup>P]dATP and 30 U 1.5  $\mu$ l AMV reverse transcriptase (Seikagaku America) in a total volume of 50  $\mu$ l. We incubated the mixture for 3 minutes at room temperature and then for 3 hours at 44°C, after which time we stopped the reaction by the addition of 2.5  $\mu$ l of 0.5 M EDTA.

We extracted the reaction mixture with an equal volume of phenol:chloroform (1:1) and precipitated the aqueous layer two times with 0.2 volume of 10 M NH<sub>4</sub>AC and 2.5 volumes EtOH and dried it under vacuum. The yield of cDNA was 1.5  $\mu$ g.

We synthesized the second strand according to the methods of Okayama and Berg [Mol. Cell. Biol., 2, p. 161 (1982)] and Gubler and Hoffman [Gene, 25, pp. 263-69 (1983)], except that we used the DNA polymerase I large fragment in the synthesis.

We blunt ended the double-stranded cDNA by resuspending the DNA in 80  $\mu$ l TA buffer (0.033 M Tris Acetate (pH 7.8); 0.066 M KAcetate; 0.01 M MgAcetate; 0.001M DTT; 50  $\mu$ g/ml BSA), 5  $\mu$ g RNase A, 4 units RNase H, 50  $\mu$ M  $\beta$  NAD, 8 units E.coli ligase, 0.3125 mM dATP, dCTP, dGTP, and dTTP, 12 units T<sub>4</sub> polymerase and incubated the reaction mixture for 90 min at

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37°C, added 1/20 volume of 0.5M EDTA, and extracted with phenol:chloroform. We chromatographed the aqueous layer on a G150 Sephadex column in 0.01M Tris-HCl (pH 7.5), 0.1 M NaCl, 0.001 M EDTA and  
5 collected the lead peak containing the double-stranded cDNA and ethanol precipitated it. Yield: 0.605 µg cDNA.

We ligated the double-stranded cDNA to linker 35/36:

10           5'AATTCGAGCTCGAGCGCGGCTGC3'  
          3'     GCTCGAGCTCGCGCGGCGG5'

using standard procedures. We then size selected the cDNA for 800 bp and longer fragments on a S500 Sephacryl column, and ligated it to EcoRI-digested  
15 bacteriophage lambda vector gt10 (a gift of Dr. Ellis Reinherz). We packaged aliquots of the ligation reaction in Gigapak (Stratagene) according to the manufacturer's protocol. We used the packaged phage to infect E.coli BNN102 cells and plated the  
20 cells for amplification. The resulting library contained  $1.125 \times 10^6$  independent recombinants.

We also screened a PBL cDNA library in the bacteriophage lambda vector gt10 (a gift of Dr. Ellis Reinherz), which was synthesized from mRNA from a  
25 T4<sup>+</sup> tumor cell line named REX, which expresses T4 protein at high levels [O. Acuto et al., "The Human T Cell Receptor: Appearance In Ontogeny And Biochemical Relationship Of Lambda and Beta Subunits on IL-2 Dependent Clones And T Cell Tumors", Cell,  
30 34, pp. 717-26 (1983)].

#### Screening Of The Libraries

We then used three of our <sup>32</sup>P-labelled synthetic oligonucleotide antisense probes, probes 3, 6 and 9, to screen in parallel our two λgt10 cDNA  
35 libraries using the plaque hybridization screening technique described in R. Cate et al., "Isolation Of

The Bovine And Human Genes For Mullerian Inhibiting Substance And Expression Of The Human Gene In Animal Cells", Cell, 45, pp. 685-98 (1986), with minor modifications. We modified the Cate et al. procedure by hybridizing without tetramethyl ammonium chloride to accommodate our use of unique probes, rather than mixtures, to probe the plaque filters.

5 We used the three probes, which had been previously 5' end-labelled with [ $\gamma$ -<sup>32</sup>P]-ATP according to the method of A. Maxam and W. Gilbert, Meth.  
10 Enzymol., 68, pp. 499-80 (1979) to screen in parallel the PBL cDNA library and the REX cDNA library discussed above.

From our screening of the PBL library, we  
15 isolated a nearly full length soluble T4 cDNA clone --  $\lambda$ 203-4 (or  $\lambda$ gt10.PBL.T4) -- containing a 3.064 kb insert which could be cleaved from the  $\lambda$ gt10 vector with EcoRI.

From our screening of the REX cell library,  
20 we isolated an incomplete T4 cDNA clone containing a 1,200 bp cDNA insert. We then further characterized the DNA from these clones by DNA sequencing analysis.

We also screened a bacteriophage lambda human genomic library, constructed in the vector  
25 EMBL3 by Dr. Mark Pasek (Biogen Inc., Cambridge, Massachusetts) [N. Murray in Lambda 2, eds. R. Hendrix, J. Roberts, F. Stahl, R. Weisberg, pp. 3935-422 (1983)]. The library contains DNA fragments, created by partial restriction of chromosomal DNA from the human lympho-  
30 blastid cell line GM1416,48, XOOX (Human Genetic Mutant Cell Repository, Camden, New Jersey) with Sau3a, ligated onto EMBL3 arms which had been subjected to cleavage with BamHI according to the procedures outlined in Maniatis et al., (1982), supra.  
35 Plating of the phage library, lysis, and transfer of the phage DNA onto nitrocellulose were performed as described by W. D. Benton and R. W. David, "Screening

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of Lambda gt Recombinant Clones By Hybridization To Single Plaques In Situ", Science, 196, p. 180 (1977) and Maniatis et al. (1982). Hybridization conditions were those described by Cate et al. (1986), supra, except that tetramethylammonium chloride (TMACl) was omitted from the washing buffer.

Approximately 2 million plaques were screened in parallel hybridizations with probe 1 and probe 3 discussed above. One phage, called CM47, which hybridized with probe 3 in the primary screenings, was subjected to DNA sequence analysis to determine the existence and position of an intron between the coding sequences for the predicted extracellular and transmembrane domains. No phage clones containing T4 sequences were found screening with probe 1, probably because it includes a sequence interrupted by an intron [D. R. Littman and S. N. Gettner, Nature, 325, pp. 453-55 (1987); and our observations].

Partial sequence analysis of CM47 shows that an intron interrupts the sequence corresponding to the codon for valine (amino acid 363) of the deduced primary sequence for T4 (Figure 3 -- in which introns are indicated by a solid line). This intron defines a potential site for introducing a stop codon in order to express a soluble form of T4. Another intron found within the coding sequence for T4 interrupts the codon for arginine (amino acid 295) and a third intron in CM47 is found between the codons for arginine (amino acid 402) and arginine (amino acid 403) (Figure 3).

#### Sequencing Of cDNA Clones

We then subcloned EcoRI digested DNA from clone  $\lambda$ 203-4 into animal expression vector pBG312 [R. Cate et al., supra] to facilitate sequence analysis. More specifically, as depicted in Figure 4,

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we then digested  $\lambda$ gt10.PBL.T4 with EcoRI to excise the 3.064 kbp EcoRI-EcoRI fragment containing the full length T4 cDNA. This cDNA sequence, including the entire coding region for soluble T4 and for full length T4 was deposited in p170-2. We used T4 ligase to ligate the fragment into animal expression vector pBG312 [supra] which had been previously cut with EcoRI, to form pBG312.T4 and p170-2 (Figure 4). We then determined the nucleotide sequence of the EcoRI fragment of pBG312.T4 using Maxam Gilbert technology [A. M. Maxam and W. Gilbert, "A New Method For Sequencing DNA", Proc. Natl. Acad. Sci. USA, 74, pp. 560-64 (1977)] (see Figure 3, which depicts the PBL cDNA sequence in comparison to that reported by Maddon et al., (1985), supra). This analysis showed that the 3.064 kbp PBL full length complementary DNA copy of T4 cDNA contained the coding sequence for T4, approximately 200 bp of 5' noncoding sequence and approximately 1500 bp of 3' noncoding sequence.

We then cut pBG312.T4 with PstI and removed the resulting 3' protruding ends with Klenow and isolated an approximately 2.5 kbp fragment. We then inserted the fragment into the polylinker of pBG312 (which had been previously restricted at the SmaI site) to form plasmid p170-2, which contains the full length PBL T4 cDNA sequence (see Figure 3).

As depicted in Figure 3, the PBL T4 cDNA contains a nucleotide sequence almost identical to the approximately 1,700 bp sequence reported by Maddon et al., (1985), supra. The PBL T4 cDNA, however, contains three nucleotide substitutions that, in the translation product of this cDNA, would produce a protein containing three amino acid substitutions compared to the sequence reported by Maddon et al. As shown in Figure 3, these differences are at amino acid position 3, where the asparagine of Maddon et al. is replaced with lysine; position 64,

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where the tryptophan of Maddon et al. is replaced with arginine and at position 231, where the phenylalanine of Maddon et al. is replaced with serine. The asparagine reported at position 3 of Maddon et al. instead of lysine was the result of a sequencing error (Dr. Richard Axel, personal communication). The significance of the amino acid replacements at positions 64 and 231, which may represent allelic polymorphism [T. C. Fuller et al., Human Immunology, 9, pp. 89-102 (1982); W. Stohl and H. G. Kunkel, Scand. J. Immunol., 20, pp. 273-78 (1984); N. Amino et al., Lancet, 2, pp. 94-95 (1984); and M. Sato et al., J. Immunol., 132, pp. 1071-73 (1984)], is not known.

DNA sequence analysis [Maxam and Gilbert, supra] of the insert in pEC100 of the REX clone suggests that it represents the product of a splicing error, because 5' noncoding sequence appears to have been spliced with coding sequence beginning with the GGT codon for glycine (amino acid 49) (see Figure 3 and Figure 5). The T4 coding sequence in pEC100\* from glycine (amino acid 49) to isoleucine (amino acid 435) is identical to the sequence of Maddon et al., (1985), supra.

In comparison, our earlier N-terminal protein sequence analysis of native T4 protein purified from U937 cells shows a T4 expression product with asparagine as amino acid 3. These differences are also set forth in Figure 6, which also depicts comparisons at corresponding positions of the partial clone from the REX cell line  $\lambda$ gt10 library; our

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\* We constructed pEC100 by digesting the incomplete T4 cDNA clone from the REX library with EcoRI and isolating the 1,200 bp cDNA insert. We then ligated it to pUC12 (Boehringer Mannheim, Indianapolis, Indiana) which had been previously cut with EcoRI to form pEC100.

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genomic clone from a  $\lambda$ EMBL3 library; mouse T4 sequences [Tourvieille et al., Science, 234, p. 610 (1986)] and sheep T4 sequences [Classon et al., Immunogenetics, 23, p. 129 (1986)].

5. Construction of Soluble T4 Mutants

We then employed the technique of in vitro site-directed mutagenesis and restriction fragment substitution to modify the T4 cDNA coding sequence of p170-2 in sequential steps to be identical to  
10 that reported by Maddon et al., (1985), supra. We first used oligonucleotide-directed mutagenesis to modify the amino acids at positions 3 and 64. Next, we employed restriction fragment substitution with a  
15 fragment including the serine 231 codon of a partial T4 cDNA isolated from a T4 positive lymphocyte cell line [O. Acuto et al., Cell, 34, pp. 717-26 (1983)] library in  $\lambda$ gt11 (a gift from Dr. Ellis Reinherz), to modify the amino acid at position 231. We then  
20 truncated our modified T4 cDNA sequence to remove the coding regions for the transmembrane and intracytoplasmic domains. Subsequently, we constructed three different soluble T4 mutants from our full length T4 clone PBL T4 by linker insertion between  
25 restriction sites in order to increase the probability of empirically finding a stable, secretable T4 molecule. The structure of each of these mutants is depicted in Figure 7A.

Line A of Figure 7A represents a hydropathy analysis of our full length soluble T4 carried out  
30 using a computer program called Pepplot (University of Wisconsin Genetics Computer Group) according to J. Kyte and R. F. Doolittle, J. Mol. Biol., 157, pp. 105-32 (1982). Line B depicts the protein domain structure of full length T4 [Maddon et al., (1985)  
35 supra] in which "S" represents the secretory signal sequence, "V" represents the immunoglobulin-like

variable region sequence, "J" represents the immunoglobulin-like joining region sequence, "U" represents the unique, extracellular region sequence, "TM" represents the transmembrane sequence and "C" represents the cytoplasmic region sequence. In line B, the transmembrane amino acid sequence and some flanking sequence is written below the TM domain. Line C depicts the protein domain structure of recombinant soluble T4 mutants rsT4.1 in pBG377, rsT4.2 in pBG380 and rsT4.3 in pBG381. Line D represents the protein domain structure of E.coli rsT4 gene (Met-perfect construct) (p199-7) which is deleted for the T4 N-terminal signal sequence (S).

We constructed the first three soluble T4 mutant gene fragments by truncating our full length soluble T4 cDNA at positions corresponding to either intron/exon boundaries or to protein domain boundaries defined by hydropathy analysis predictions. More specifically, we introduced synthetic linkers into the unique AvaI site that is 5' to the transmembrane/extracellular domain boundary to produce an in-frame translational stop codon, thus constructing T4 genes that lack the transmembrane and cytoplasmic domains of the full length T4 sequence.

For example, mutant rsT4.1 in pBG377 was truncated by the insertion of a stop codon following amino acid 362, lysine, which corresponds to the position of an intron separating the extracellular and transmembrane domain exons. The positions both of this intron and of the adjacent intron that splits the transmembrane and cytoplasmic domains were determined by DNA sequence analysis of chromosomal T4 clones isolated from the  $\lambda$ EMBL3 genomic library described above. Although the significance of the intron positions flanking the T4 transmembrane domain is not known, the determination of the genetic structure could provide important information for design-

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ing rsT4 mutants, since exons frequently define functional domains [W. Gilbert, "Why Genes In Pieces?", Nature, 271, p. 501 (1978)].

We then constructed mutant rsT4.2 in pBG380  
5 by truncating the T4 cDNA at the boundary of the transmembrane and extracellular domains at amino acid 374. And, we constructed mutant rsT4.3 in pBG381 by truncating the T4 cDNA at amino acid 377, three amino acids downstream from the transmembrane/  
10 extracellular domain boundary and within the transmembrane domain.

We also employed the technique of oligonucleotide site directed mutagenesis, according to D. Strauss et al., "Active Site Of Triosephosphate  
15 Isomerase: In Vitro Mutagenesis And Characterization Of An Altered Enzyme", Proc. Natl. Acad. Sci. USA, 82, pp. 2272-76 (1985), to construct a fourth soluble T4 mutant from our full length T4 clone PBL T4. The structure of this mutant is depicted in Figure 7A,  
20 line D, which represents the protein domain structure of E.coli rsT4 gene (Met-perfect rsT4.2) construct, deposited in p199-7, which is deleted for the T4 N-terminal signal sequence (S).

We also constructed various other soluble  
25 T4 deletion mutants to determine which smaller fragments of the T4 sequence provide a protein which binds to HIV. These constructions were based on our belief that only the amino terminal sequence of T4 is required for binding to HIV. This belief, in turn,  
30 was based upon observations that the monoclonal antibody OKT4A blocks infection of T4 positive cells by HIV and it appears to recognize an epitope in the amino portion of T4 [Fuller et al., supra]. Such fragments of T4, which lack glycosylation and which  
35 are capable of binding HIV and blocking infection, may be produced in E.coli or chemically synthesized.

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The structure of each of these deletion mutants is depicted in Figure 7B. In that figure, line A depicts the protein domain structure of full length T4 [Maddon et al., (1985), supra; Figure 7A].

5 In line B, the protein structure of recombinant soluble T4 mutants are depicted as follows: rsT4.7 in p203-5, rsT4.7 in pBG392, rsT4.8 in pBG393, rsT4.9 in pBG394, rsT4.10 in pBG395, rsT4.11 in pBG397, rsT4.12 in pBG396, rsT4.111 in pBG215-7, rsT4.113.1  
10 in pBG211-11 and rsT4.113.2 in pBG214-10.

We constructed soluble T4 derivatives p203-5, pBG392, pBG393, pBG394 and pBG396 by truncating our rsT4.2 gene after the StuI sites at amino acids 183 and 264 of rsT4.2. More specifically, we  
15 constructed derivative rsT4.7 in p203-5 and in pBG392 by truncating the rsT4.2 cDNA at amino acid 182. And, we constructed each of derivatives rsT4.9 in pBG394 and rsT4.12 in pBG396 by truncating the rsT4.2 cDNA at amino acids 113, and 166, respectively. One  
20 may also construct each of derivatives rsT4.10 in pBG395 and rsT4.11 in pBG397 by truncating the rsT4.2 cDNA at amino acids 131 and 145, respectively.

#### Expression of T4 and Soluble T4 Polypeptides In Bacterial Cells

25 The cDNA sequences of this invention can be used to transform eukaryotic and prokaryotic host cells by techniques well known in the art to produce recombinant soluble T4 polypeptides in clinically and commercially useful amounts.

30 For example, we constructed expression vector p199-7, as shown in Figure 9A, as follows.

We preceded the construction depicted in Figure 9A by the construction of various intermediate plasmids, as depicted in Figures 8A-8D. Those con-  
35 structions were carried out using conventional

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recombinant techniques. The linkers employed in those constructions are set forth in Figure 10.

As depicted in Figures 8A and 8B, starting with p170-2, which contains our full length T4 DNA sequence, coding for T4 characterized by three different amino acids than that of Maddon et al., (1985), supra, we produced various constructs which direct the expression of soluble T4. Some of these constructs are characterized in that one or more of those amino acid differences have been changed to correspond to the respective amino acids of Maddon et al. In this figure, as well as in the other figures, amino acid changes are reflected by an arrow.

Plasmid p192-6 contains the Met perfect rsT4.2 sequence derived by oligonucleotide site-directed mutagenesis which removed the entire T4 N-terminal signal sequence as shown in Figure 8C. And, to provide a convenient means of transferring the rsT4.2 Met perfect sequence into E.coli expression vectors, the steps described in Figure 8D were carried out to produce p195-8, a plasmid containing the Met perfect rsT4.2 sequence flanked by ClaI restriction sites. The ClaI-ClaI cassette of p195-8 optimizes the distance between the 5' ClaI site and the initiating Met codon. In Figure 8D, ST8 rop<sup>-</sup> is a tetracycline resistance encoding pAT153-based plasmid containing the rop<sup>-</sup> mutation that permits high plasmid copy number, a promoter and ribosome binding site from bacteriophage gene 32 and the gene 32 transcription termination sequence.

Cleavage of p195-8 with ClaI produced the fragment used to assemble p199-7, a construction which directs the expression of Met perfect rsT4.2 under the control of the P<sub>L</sub> promoter (Figure 9A). As the first step, to construct a vector from which rsT4.2 expression is under control of the P<sub>L</sub> promoter,

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we constructed the vector p197-1<sup>2</sup> from p1034 (plmuGCSF) (Figure 9A).

5 We then cut p1034 with EcoRI and BamHI to excise the GCSF cDNA insert and a portion of the phage mu ribosome binding site sequence -- which we subsequently reconstructed with oligonucleotides. The synthetic linkers used were linkers 57-60 (Figure 10).

10 We then ligated the synthetic linker into the EcoRI/BamHI-cut p1034 to form p197-12. One could, instead, replace these steps by starting with any suitable E.coli expression vector containing a Clai site appropriately placed between the promoter and terminator sequences. We cut p197-12 with Clai and  
15 inserted a Clai-Clai cassette containing the cDNA sequence of rsT4.3 in pBG381 and phage transcription terminator derived from p1034. The sequence of this cassette is depicted in Figure 11. The resulting plasmid, p199-7, contains the rsT4.2 "Met perfect"  
20 gene in that vector.

Alternatively, one could derive the Met perfect rsT4.2 sequence from plasmid pBG380, deposited in connection with this application, and gap out the signal sequence to create p192-6.

25 We tested for expression of p199-7 as follows. SG936, an E.coli lon htp<sub>r</sub> double mutant [ATCC 39624] [S. Goff and A. Goldberg, "ATP-Dependent Protein Degradation In E.coli", in Maximizing Gene Expression, W. Reznikoff and L. Gold (eds.) (1986)],  
30 was transformed with p199-7 by conventional procedures [Maniatis et al. (1982)] to form SG936/p199-7, a transformant containing a plasmid with the Met-perfect rsT4.2 gene behind the P<sub>L</sub> promoter. Transformants were selected on LB agar plates containing  
35 10 mcg/ml tetracycline (tet). After streaking out several single colonies for single colony isolation, one was chosen at random for testing induction of

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rsT4.2 synthesis. We picked a single colony from an LB-agar tet<sup>+</sup> plate into 20 ml Luria Broth (LB) and 10 mcg/ml tet in a 125 ml shake flask and grew it overnight in a shaking air incubator (New Brunswick Scientific, New Jersey) at 30°C.

We then initiated an induction culture by adding 0.5 ml of the overnight culture to 50 ml LB and tet in a 500 ml flask which was grown at 30°C in a shaking air incubator. When the culture reached an OD(600) of 0.4, we transferred it to a 42°C water-bath and shook it gently for approximately 20 minutes. After heat induction at 42°C, the flask was transferred to a 39°C air incubator (New Brunswick Scientific, New Jersey) where it was shaken vigorously at 250 rpm. We withdrew samples just after the 42°C heat shock, and at hourly time points for 4 hours, and then after overnight growth. The samples were measured for growth by OD(600) and analyzed following SDS-PAGE for the pattern of protein synthesis by Coomassie blue protein staining and by Western blot analysis with our rabbit anti-peptide antibody probes (described above). Based on the relative molecular weight and protein blot analysis, the expression of rsT4.2 was induced from SG936/p199-7 following heat induction at 42°C (Figure 12).

We transformed p199-7 into a P<sub>L</sub>mu.tet expression vector, an E.coli expression vector, at the unique Clal site (see Figure 11). The nucleotide and amino acid sequences of p199-7 are shown in Figure 11.

The expression of soluble T4 from p199-7 in E.coli was measured by Western blot analysis of whole cell extracts following SDS-PAGE using the rabbit polyclonal anti-peptide JB-1 or anti-peptide JB-2 antibodies as probes (Figure 12).

We also constructed expression vector p203-5, as shown in Figure 9B, as follows.



We started with p197-7, which has the same sequence as the P<sub>L</sub>um vector p197-1 (see Figure 9A), except that there is a single nucleotide deletion in the 5' noncoding region following the P<sub>L</sub> promoter.

5 That deletion, which is a deletion of nucleotide #40 -- adenine -- of p197-12 (see Figure 11), resulted from a deletion in the region that was constructed from linkers 57-60 (see Figure 10). p197-7 contains the rsT4.2 gene comprising 374 amino acids. Alternatively, one could also use p197-7 as a starting plasmid.

We cut p197-7 with ClaI. We also cut p195-8 (see Figures 8D and 9A) with ClaI to remove the ClaI - ClaI cassette containing the cDNA sequence of rsT4.2. Subsequently, we inserted the ClaI-ClaI cassette into p197-7 to produce p198-2.

We then digested p198-2 with StuI to remove 80 amino acids (amino acid 185 to amino acid 264) of the mature T4 protein coding sequence. Unexpected methylation, however, prevented cutting at the second StuI site, so that only the StuI site at amino acid 184 was cleaved. Following ligation, the plasmid DNA was transformed into E.coli and we examined several plasmid clones for the deletion using standard procedures. None of those plasmids contained the expected StuI deletion.

Subsequent DNA sequence analysis of one of these plasmids, called p203-5, showed that two guanine residues (see amino acids 183 and 184; nucleotides 818 and 819 of Figure 3) of the StuI recognition sequence had been deleted following cleavage due to exonuclease digestion caused by the use of exonuclease-contaminated StuI enzyme. This dinucleotide deletion produced a translation frameshift following amino acid 182 (glutamine) and introduced a stop codon six amino acid codons downstream from the frameshift (Figure 9C). The unexpected

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methylation of the second StuI site together with the deletion that resulted in a few stop codon produced a gene encoding a shortened form of recombinant soluble T4, called rsT4.7. The rsT4.7 sequence  
5 encodes a 182 amino acid N-terminal segment of the mature T4 sequence followed by, at the C-terminus, six amino acids -- asparagine-leucine-glutamine-histidine-serine-leucine -- of non-T4 sequence and finally by a TAA stop codon.

10 The expression of soluble T4 from p203-5 in E.coli was measured by Western blot analysis as previously described.

Expression of T4 and Soluble T4  
Polypeptides In Animal Cells

15 We inserted both soluble T4 genes and the unmodified gene encoding membrane-bound T4 into animal expression vector pBG368. More specifically, we inserted each of the soluble gene constructs into pBG368 under the transcriptional control of the  
20 adenovirus late promoter, to give plasmids pBG377, pBG380 and pBG381. We also made two pBG312-based constructions, called pBG378 and pBG379, which direct the expression of recombinant full length T4 protein. pBG378 and pBG379 code for the same full  
25 length T4 protein but in pBG379, a portion of the 3' untranslated sequence has been removed. Subsequently, to test for expression of recombinant soluble T4 and recombinant full length T4, we cotransfected Chinese hamster ovary ("CHO") cells with one of each of  
30 those plasmids and with the plasmid pAdD26.

We first constructed pBG368 as follows. As depicted in Figure 13, we cut animal cell expression vector pBG312 [R. Cate et al., "Isolation Of The Bovine And Human Genes For Mullerian Inhibiting  
35 Substance And Expression Of The Human Gene In Animal Cells", Cell, 45, pp. 685-98 (1986)] with EcoRI and

BglII to delete one of each of the two EcoRI and the two BglII restriction sites (the EcoRI site at position 0 and the BglII site located at approximately position 99). The resulting plasmid, pBG368, retained  
5 an EcoRI site in the cloning region and a BglII site after the cloning region. This left a single EcoRI site and a single BglII site in the polylinker for cloning purposes.

More specifically, we deleted one EcoRI  
10 site and one BglII site by sequential partial digestion of pBG312 with restriction enzymes EcoRI and BglII, respectively. We filled in with Klenow and 4 nucleotides then religated to produce pBG368, which contains unique restriction sites for EcoRI and BglII  
15 enzymes.

Once transient expression of soluble T4 was verified, we constructed stable cell lines that continuously expressed soluble T4. To do this, we employed the stable cell expression host, the  
20 dihydrofolate reductase deletion mutant (DHFR<sup>-</sup>) Chinese hamster ovary cell line [F. Kao et al., "Genetics Of Somatic Mammalian Cells X Complementation Analysis of Glycine-Requiring Mutants", Proc. Natl. Acad. Sci., 64, pp. 1284-91 (1969); L. Chasin and  
25 G. Urlab "Isolation Of Chinese Hamster Cell Mutants Deficient In Dihydrofolate Reductase Activity", Proc. Natl. Acad. Sci., 77, pp. 4216-80 (1980)].

Using this system, we cotransfected each T4 gene construct with pAdD26 [R. J. Kaufman and  
30 P. A. Sharp, "Amplification And Expression Of Sequences Cotransfected With a Modular Dihydrofolate Reductase Complementary DNA Gene", J. Mol. Biol., 159, pp. 661-21 (1982) containing the mouse DHFR gene. Before carrying out the co-transfections, we  
35 linearized all plasmids by restriction enzyme cleavage and, prior to transfection, we mixed each plasmid with pAdD26 so that the molar ratio of pAdD26 to T4

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was 1:10. This maximized the number of T4 gene copies per transfectant.

Within the cell, the plasmids were ligated together to form polymers that can become integrated into host chromosomal sequences by illegitimate recombination [J. Haynes and C. Weissmann, "Constitutive, Long-Term Production Of Human Interferons By Hamster Cells Containing Multiple Copies Of a Cloned Interferon Gene", Nucl. Acids Res., 11, pp. 687-706 (1983); S. J. Scabill et al., "Expression And Characterization Of The Product Of A Human Immune Interferon cDNA Gene In Chinese Hamster Ovary Cells", Proc. Natl. Acad. Sci. USA, 80, pp. 4654-58 (1983)]. We selected transfectants that express the mouse DHFR gene in culture medium lacking nucleotides. We then subjected these transfectants to a series of increasing concentrations of methotrexate, a toxic folate analogue that binds DHFR, to select for cells levels of DHFR.

Resistance to methotrexate by increased expression of DHFR is frequently the result of DHFR gene amplification, which can include the reiteration of large chromosomal segments, called amplified units [R. J. Kaufman and P. A. Sharp, "Amplification And Expression Of Loss Of Dihydrofolate Reductase Genes In A Chinese Hamster Ovary Cell Line", Molec. Cell. Biol., 1, pp. 1069-76 (1981)]. Therefore, cointegration of DHFR and rsT4 sequences permitted the amplification of rsT4 genes. Stably transfected cell lines were isolated by cloning in selective growth medium, then screened for T4 expression with a T4 antigen (RIA) [D. Klatzmann et al., Nature, 312, pp. 767-68 (1984)] and by immunoprecipitation from conditioned medium after [<sup>35</sup>S] cysteine ("<sup>35</sup>S-Cys") metabolic labelling.

We also inserted the soluble T4 derivative rsT4.7 gene into an animal cell expression plasmid as follows.

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As set forth in Figure 14C, we cut plasmid pBG381 (Figure 14A) with EcoRI and NheI. We then cut p186-6 with EcoRI and NheI to remove the 786 base pair fragment. We ligated that fragment into the digested pBG381 to form plasmid pBG391. The T4 sequence in pBG391 is identical to both that of Maddon et al. (1985) supra at positions 64 (tryptophan) and 231 (phenylalanine) and to that of pBG381. However, at position 3, the asparagine reported by Maddon et al. and present in pBG381 is replaced with lysine. The nucleotide sequence of pBG391 is depicted in Figure 15.

We then digested p203-5 with NheI and OxaI to remove the 483 base pair fragment. We inserted that fragment into NheI/OxaI-digested pBG391 to form plasmid pBG392, the animal cell expression construct of rsT4.7. The T4 sequence in rsT4.7 contains amino acids identical to that of Maddon et al.'s full length sequence at amino acid positions 64 (tryptophan) and 231 (phenylalanine). However, at position 3, the asparagine reported by Maddon et al. is replaced with lysine. The nucleotide sequence of pBG392 is depicted in Figure 16.

In Figure 14D, we have depicted the construction of other animal cell expression constructs containing sequences encoding the deletions rsT4.9 in pBG394, and rsT4.12 in pBG396. Those constructions were carried out using conventional recombinant techniques. The linkers employed in those constructions are set forth in Figure 18. The nucleotide sequences of pBG394 and pBG396 are shown in Figures 19 and 20.

Plasmid pBG393, shown in Figure 17, contains rsT4.8, the perfect form of rsT4.7. pBG393 contains 182 amino acids of the mature T4 sequence, without the additional non-T4 6 amino acids at the C-terminus following amino acid 182. The nucleotide sequence of BG393 is shown in Figure 21.

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Other animal cell expression plasmids according to this invention may be constructed as depicted in Figure 17. These include rsT4.10 in pBG395 and rsT4.11 in pBG397 (see Figure 18 for specific linkers).

The nucleotide sequence of BG395 is shown in Figure 22.

#### Purification Of Recombinant Soluble T4

Recombinant soluble T4 construct pBG380 expressed in DHFR<sup>-</sup> CHO cells was grown to confluency in a  $\alpha$ -Modified Eagles Medium (Gibco) supplemented with 10% fetal calf serum, 1 mM glutamine and the antibiotics penicillin and streptomycin (100  $\mu$ g/ml of each). The cells were grown at 37°C in two 21 Cell Factory Systems (Nunc). We then washed the confluent cells free of fetal calf serum with  $\alpha$ -Modified Eagles Medium without fetal calf serum and cultured the cells in  $\alpha$ -Modified Eagles Medium at 37°C for 4 days. Subsequently, we harvested the conditioned media, filtered it through a Millipore Millidisk 0.22 $\mu$  hydrophilic filter cartridge (Millipore #MCGL 305-01) and concentrated the secreted proteins on a fast-S ion exchange column (S-Sepharose Fast Flow, Pharmacia #17-0511-01) in 20 mM MES buffer (pH 5.5).

We then eluted the bound proteins with 20 mM Tris-HCl (pH 7.7) and 0.3 M NaCl. The elution pool was subsequently diluted with 2 volumes of 20 mM Tris-HCl (pH 7.7) and it was then loaded on a column comprising immobilized 19Thy anti-T4 monoclonal antibody coupled to Affigel-10 [a gift of Dr. Ellis Reinherz, Dana Farber Cancer Institute, Boston, Massachusetts]. We washed the column extensively and eluted the bound material as 0.5 ml fractions with 50 mM glycine-HCl (pH 2.5), 150 mM NaCl, 0.1 mM EGTA and 5  $\mu$ g/ml bovine pancreatic trypsin inhibitor, Aprotinin (Sigma #A1153). We used Western blots

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developed with rabbit antisera raised against peptide JB-2 to follow the purification. We employed silver stained gels to follow binding and elution of rsT4.2 during the chromatography. Figure 23 depicts a

5 Coomassie stained gel of purified rsT4.2.

Gel sizing-column chromatography analysis of the purified rsT4.2 from the pBG380 transfected CHO cell line, BG380G, suggests that rsT4 is monmeric under physiologic pH and salt concentration.

10 Sequencing Of Recombinant Soluble T4 Protein

We then determined the N-terminal amino acid sequence of a recombinant soluble T4, specifically rsT4.2, molecule purified from the conditioned  
15 medium of the pBG380 transfected CHO cell line BG80G, as described above, by automated Edman degradation in an Applied Biosystems 470A gas phase sequenator [R. B. Pepinsky et al., J. Biol Chem., 261, pp. 4239-46 (1986)].

20 The amino terminal sequence matched the sequence which we had previously determined for solubilized native T4 isolated from U937 cells, supra. The amino terminal sequences of native solubilized T4 (sT4) and purified rsT4 protein are  $\Delta 2$  proteins,  
25 as compared to the amino terminal sequence predicted by Maddon et al., (1985), supra, with the mature amino terminus located at position 3 of that sequence. The amino terminal sequences of solubilized native T4 (sT4), recombinant soluble T4 (rsT4.2) secreted by  
30 CHO transfectant BG380G containing pBG380 and the protein sequence deduced by Maddon et al. (1985), supra are as follows:

sT4:	X-K-V-V-L-X-K-K-X-D-T-V-E-L-T-X-T-A-S-E-
rsT4.2:	N-K-V-V-L-G-K-K-G-D-T-V-E-L-T-X-T-A-S-E-

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Maddon  
et al.

Q-G-N-K-V-V-L-G-K-K-G-D-T-V-E-L-T-C-T-A-S-E

In the above sequences, the amino acids  
are represented by single letter codes as follows:

5        Phe: F    Leu: L    Ile: I    Met: M  
         Val: V    Ser: S    Pro: P    Thr: T  
         Ala: A    Tyr: Y    His: H    Gln: Q  
         Asn: N    Lys: K    Asp: D    Glu: E  
         Cys: C    Trp: W    Arg: R    Gly: G

10        X: not determined or ambiguous.

We also constructed pBG211-11, a plasmid  
coding for the N-terminal 113 amino acids of soluble  
T4 protein. This construct, which codes for a pro-  
tein characterized by a single disulfide bridge,  
15        between the cysteines at amino acid positions 18 and  
86, is conveniently expressed in E.coli.

To construct p211-11, as depicted in Fig-  
ure 24, we first cut p195-8 (see Figures 8D and 9A)  
with ClaI to remove the ClaI-ClaI cassette contain-  
20        ing the cDNA sequence of rsT4.2. We then digested  
pAT153y3SH16AAmp, the tryptophan operon promoter  
plasmid from the gamma interferon producing E.coli  
strain BN374 with ClaI, and deleted the cDNA coding  
for gamma interferon. Subsequently, we inserted  
25        the ClaI-ClaI cassette into the ClaI-cut E.coli  
plasmid in front of the tryptophan operon promoter  
and ligated to produce p196-10.

As shown in Figure 25, we then subjected  
pBG380 to oligonucleotide-directed mutagenesis to  
30        insert three tandem translational stop codons follow-  
ing the T4 cDNA sequence coding for amino acids -23  
to 113 in pBG380, to produce pBG394.

We then constructed p211-11 from fragments  
of each of p196-10, pBG394 and p1034 as depicted in  
35        Figure 26. The first fragment including the vector  
sequences, was produced by restricting p196-10 with

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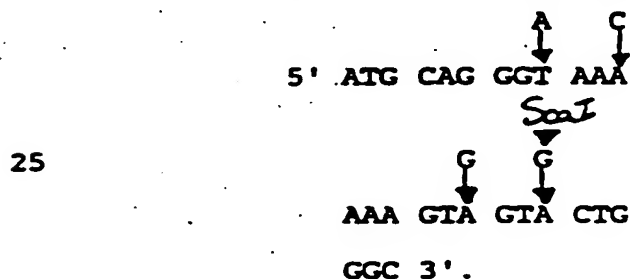
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HindIII and ClaI to remove the T4 coding sequence from amino acids 61 through 374 of rsT4.2 and including vector sequence following the 3' end of the rsT4 gene. The second fragment, a HindIII - BglII segment including the codons for T4 amino acids 61-113 of rsT4.9 immediately followed by a triplet of stop codons in tandem, was isolated by HindIII/BglII digestion of pBG394. The third fragment, a BamHI - ClaI fragment containing a bacteriophage T4 transcriptional termination signal [H. N. Kirsch and B. Allet, "Nucleotide Sequences Involved In Bacteriophage T4 Gene 32 Translational Self-Regulation", Proc. Natl. Acad. Sci. USA, 79, pp. 4937-41 (1982)], was isolated by BamHI/ClaI digestion of p1034. We then ligated these three fragments to produce p211-11, a T4 construct coding for a 113 amino acid soluble form of T4 protein, with asparagine at amino acid position 3 (i.e., rsT4.113.1).

We then subjected p211-11 to oligonucleotide site-directed mutagenesis (Figure 27) to change the amino acid at position 3 from asparagine to lysine using the oligonucleotide T4-66:



This produced plasmid p214-10, a fully corrected 113 amino acid soluble T4 vector coding for a 113 amino acid soluble form of T4 protein, with lysine at amino acid position 3 (i.e., rsT4.113.2). As shown in Figure 27, we subjected p214-10 to oligonucleotide site-directed mutagenesis to delete glutamine and glycine at, respectively,

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amino acid positions 1 and 2 of the T4 sequence using the oligonucleotide T4AID-87:

C  
↓

5' GTA TCG ATT TGG  
ATG ATG AAA AAA  
GTA GTA 3'.

This produced p215-7, a 111 amino acid soluble T4 construct, including the trp promoter, which directs the expression of a 111 amino acid soluble form of T4 protein, with lysine at amino acid position 3 (i.e., rsT4.111).

We next constructed p218-8, a 111 amino acid construct which directs the expression of a 111 amino acid soluble form of T4 protein, with lysine at amino acid position 3 (i.e., rsT4.111) under the control of the  $P_L$  promoter, as depicted in Figure 28.

More specifically, we cut p197-12 (Figure 9A) with ClaI to remove the 101 bp fragment containing linker and terminator sequences. We also cut p215-7 with ClaI to remove the ClaI - ClaI cassette containing the cDNA sequence of rsT4.111 and the  $\phi$ T4 transcriptional terminator sequence [Kirsch and Allet, supra]. Subsequently, we inserted the ClaI - ClaI cassette into the ClaI-cut p197-12 to produce p218-8.

In order to express rsT4.113.1, we transformed E.coli A89 with p211-11 by conventional techniques [Maniatis et al. (1982), supra] to form E.coli A89/p211-11. E.coli A89 is a tetracycline sensitive derivative of E.coli SG936. We isolated E.coli A89 from E.coli SG936 according to the method of S. R. Maloy and W. D. Nunn, "Selection For Loss Of Tetracycline Resistance By Escherichia coli", J. Bact., 145, pp. 110-12 (1981), which is based upon the ability of the lipophilic chelating agent fusaric acid to selectively inhibit resistant strains.

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More specifically, we plated E.coli SG936 on medium containing, per liter, 5 g tryptone, 5 g yeast extract, 10 g NaCl, 10 g  $\text{NaH}_2\text{PO}_4 \cdot \text{H}_2\text{O}$ , 50 mg chlortetracycline-HCl, 12 mg fusaric acid, 0.1 mM  $\text{ZnCl}_2$  and 15 g agar. Colonies which grew at 30°C (putative tetracycline-sensitive strains) were retested for tetracycline sensitivity on L-agar plates containing 5 µg/ml tetracycline. One tetracycline-sensitive strain, designated A89, was then shown to be unable to grow on LB agar at 42°C, thus verifying the presence of the htpR mutation.

Transformants were selected by tetracycline resistance. We picked a single colony into 20 ml of minimal medium plus 0.2% casamino acids plus tryptophan (100 µg/ml) plus tetracycline (10 µg/ml) in a 100 ml shake flask placed in a shaking air incubator at 30°C and allowed the cells to grow up overnight. The following morning, we inoculated 40 ml of minimal medium plus 0.2% casamino acids plus tryptophan (100 µg/ml) plus tetracycline (10 µg/ml) with the overnight culture at  $\text{OD}_{600} = 0.05$  in a 500 ml flask. The cells were grown to midlog phase and then induced by pelleting, washing once in minimal medium and then resuspending in minimal medium plus 0.2% casamino acids plus tetracycline (10 µg/ml), in the absence of tryptophan. We removed 0.6  $\text{OD}_{600}$  of cells after 0, 1, 2, 3 and 4 hours incubation and after growth overnight.

The aliquots were centrifuged and cell pellets were subjected to lysis by boiling in Laemmli gel loading buffer. After centrifugation to remove cell debris, half of each sample was subjected to SDS-PAGE, followed by Western blot analysis with our rabbit antipeptide antibody probes or by Coomassie blue protein staining (Figures 29A and 29B).

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Purification Of rsT4.113.1

We then purified rsT4.113.1 from the E.coli transformant by means of two essentially quantitative steps involving anion-exchange and gel-filtration chromatographies performed under reducing and denaturing conditions.

More specifically, we suspended 14 g of wet cells from a 4 L shake-flask fermentation in 100 ml of a 20mM Tris (pH 7.5) buffer containing 20 µg/ml DNase, 20 µg/ml RNase and 1 mM phenylmethylsulfonylfluoride ("PMSF"). The suspension was applied to a French Press at 1000 psi in two passages and then centrifuged in an SA 600 rotor at 18,000 g for 15 min at 4°C. The resulting pellet was solubilized in 20 ml of a 20 mM Tris (pH 7.5) buffer containing 7 M urea and 10 mM 2-mercaptoethanol. We then subjected the suspension to ultracentrifugation at 85,000 g for 90 min at 4°C. The supernatant was diluted by the addition of 80 ml of 20 mM Tris (pH 7.5) buffer containing 7 M urea and 10 mM 2-mercaptoethanol and 40 ml of the sample was applied to a 3 x 4 cm Q-Sepharose fast-flow column (Sigma, St. Louis, Missouri) which had been pre-equilibrated in the same buffer. The column was developed with a gradient in 400 ml total volume of increasing NaCl from 0 to 0.3 M in the same Tris/urea/2-mercaptoethanol buffer. Column fractions were monitored for absorbance at 280 nm and for protein content by SDS-PAGE (15% acrylamide). The fractions were also analyzed by Western blots. Figure 30, panel (a) is a chromatogram displaying the purification of rsT4.113.1 by ion-exchange chromatography. In that figure, peaks containing rsT4.113.1 are identified. The rsT4.113.1 was found to elute early in the NaCl gradient and to be well-resolved from low-molecular weight contaminants.

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In order to separate rsT4.113.1 from high-molecular weight contaminants, we carried out gel-filtration chromatography on an rsT4.113.1-containing pool for final purification of the protein to near  
5 homogeneity (>95% purity). More specifically, we prepared a pool containing 20 mg of protein in 50 ml and then concentrated to 10 ml in a stirred-cell ultrafiltration unit (Amicon, Danvers, MA.) using a PM-30 membrane (Amicon). Subsequently, 5.0 ml of  
10 the concentrate was applied to a 1.5 x 95 cm S-300 column (Sigma) equilibrated and developed in the same Tris/urea/2-mercaptoethanol buffer. We monitored the column fractions for absorbance at 280 nm and for protein content by SDS-PAGE. The fractions  
15 were also analyzed by Western blots. A pool containing rsT4.113.1 (approximately 4 mg) in 15 ml was thus prepared. Figure 30, panel (b) is a chromatogram displaying the purification of rsT4.113.1 by gel-filtration separation of the rsT4.113.1 pool.  
20 In that figure, peaks containing rsT4.113.1 are identified.

Figure 30, panel (c) is an SDS-PAGE analysis depicting the purification of the rsT4 derivative throughout the centrifugation and chromatography  
25 steps. In Figure 30, panel (c), the lanes depicted are:

lane A: molecular weight standards  
lane B: cell extracts  
lane C: cell pellet following solubilization  
30 of cell extract in non-denaturing conditions  
lane D: supernatant following solubilization of cell extract in non-denaturing buffer  
35 lane E: supernatant following ultracentrifugation step

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lane F: Q-Sepharose pool  
lane G: S-300 gel-filtration pool.

#### Refolding Of Purified rsT4.113.1

We refolded the purified rsT4.113.1 by  
5 dilution and dialysis steps to non-denaturing and  
oxidized conditions. More specifically, refolding  
of the protein at a concentration of 0.5 OD (280)/ml  
was achieved by stepwise dialysis against 500 volumes  
of 3 M urea, 20 mM Tris (pH 7.5); 500 volumes of 1 M  
10 urea, 0.1 M ammonium acetate (pH 6.8) and, finally,  
the same volume of a phosphate-buffered saline solu-  
tion. Throughout the refolding procedure, samples  
of the protein were monitored for relative content  
by spectral analysis and by high-performance liquid  
15 chromatography ("HPLC") performed on a 150A liquid  
chromatographic system (Applied Biosystems, Inc.,  
Foster City, California). An octasilyl column  
(Aquapore RP-300, 0.46 x 3.0 cm) was equilibrated in  
80% 0.1% trifluoroacetic acid ("TFA")/water (sol-  
vent A) and 20% 0.085% TFA/70% acetonitrile (sol-  
vent B) and developed with a linear gradient of  
20 increasing acetonitrile concentration from 20% to  
80% (solvent B) over 45 min at a flow rate of  
0.5 ml/min.

25 As shown in Figure 31, panel (a), protein  
in 7 M urea, 10 mM 2-mercaptoethanol and 20 mM  
Tris(pH 7.5) eluted from the HPLC column at 49%  
acetonitrile in the gradient. In subsequent steps,  
from 1 M urea/1 mM ammonium acetate (pH 6.8) [Fig-  
30 ure 31, panel (b)] to phosphate buffered saline  
[Figure 31, panel (c)], an increasing percentage of  
rsT4.113.1 was found to elute earlier in the HPLC  
gradient -- at 47% acetonitrile. The identity of  
the earlier eluting peak as oxidized product was  
35 verified by reduction of rsT4.113.1 in non-chaotropic

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solutions and application of sample thus treated to HPLC under the same conditions.

5 The elution of oxidized rsT4.113.1 prior to reduced protein on HPLC suggests that formation of the single disulfide bridge decreases relative hydrophobicity of the protein [J. L. Browning et al., Anal. Biochem., 155, pp. 123-28 (1986)]. Spectral analysis of rsT4.113.1 was performed throughout the course of refolding in order to monitor relative yield of soluble protein in the procedure. The refolding method allowed approximately 20% recovery of rsT4.113.1. HPLC analysis indicated a less than 15% contaminant of reduced protein in the preparation (Figure 30, panel (c), lane G).

15 Sequencing Of Renatured rsT4.113

We then carried out amino acid analysis of rsT4.113.1 by automated Edman degradation in an Applied Biosystems 470A gas phase sequenator equipped with a 900 A data system. Phenylthiohydantion amino acids generated during the course of the degradative chemistry were analyzed on-line using an Applied Biosystems 120A PTH-analyzer equipped with a PTH-C18 2.1 x 220 mm column. Protein (10 µg) for sequence analysis was applied to SDS-PAGE (15% acrylamide) and electroblotted on an Immobilon membrane (Millipore Corp., Bedford, Massachusetts) as described by P. Matsudaira, J. Biol. Chem., 262, pp. 10035-38 (1987).

Amino acid analysis of protein samples was performed by hydrolysis of protein in 6 N HCl, in vacuo, for 24 h at 110°C. The hydrolysates were then applied to a Beckman 6300 Analyzer equipped with post-column detection by ninhydrin. Western blot analysis of the SDS-PAGE gels was carried out by standard techniques using rabbit antisera JB-1.

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Sequence analysis revealed an amino terminal sequence of: Met-Gln-Gly-Asn-Lys-Val-Val ...

5 The purified rsT4.113.1 protein was found to contain stoichiometric quantities of the amino-terminal methionine placed in the protein construct for expression in E.coli and an intact polypeptide chain consistent with a sequence derived from the plasmid construction. Recovery of phenylthiohydantoinyl-methionine at the first cycle of the degradative chemistry was 60% consistent with routine initial yields obtained in the automated Edman. This observation excludes the possibility that a significant percentage of the rsT4.113.1 lacked the initiation methionine, i.e., the NH<sub>2</sub>-methionine was not removed by expression of rsT4.113.1 in E.coli, or that sequence analysis was impaired by the presence of glutamine at the first cycle of the degradative chemistry. Sequence analysis was performed for 40 cycles and no evidence of lysine carbamylation was observed. Amino acid analysis displayed a close correlation of actual and theoretical values for amino acids, thus indicating the marked absence of proteolytic degradation in the course of expression, or purification, or both.

25 Immunoprecipitation Of CHO Cell Lines Producing Soluble T4

We tested the conditioned media from <sup>35</sup>S-Cys metabolically labelled CHO cells transfected with one of the T4 mutant constructs pBG377, pBG380, pBG381, the full length recombinant T4 construct pBG379, of this invention or vector only, to determine whether any produced a molecule recognized by the anti-T4 monoclonal antibody 19 Thy. To carry out this test, we incubated about 10<sup>7</sup> CHO cells transfected with either pBG380, pBG381, pBG377, pBG379 or pBG312, for 35 5 hours at 37°C with 180 µCi/ml <sup>35</sup>S-labelled cysteine

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[DuPont, New England Nuclear] in 4 ml RPMI cys<sup>-</sup> medium (Gibco). After labelling of the cells, 1 ml of filtered, conditioned media was made 0.5 mM with phenyl-methyl-sulphonyl fluoride and immunoprecipitated with OKT4 and protein A Sepharose [P. H. Sayre and E. L. Reinherz, Eur. J. Immunol., 15, pp. 291-95 (1985)]. Subsequently, we incubated media from the <sup>35</sup>S-labelled cells with OKT4 (ATCC #CRL 8002). We then immuno-precipitated with protein A Sepharose and subjected the immuno-precipitates to SDS-PAGE under reducing conditions on 10% polyacrylamide gels [U. K. Laemmli, Nature, 227, pp. 680-85 (1980)]. Autoradiography was carried out with X-Omat X-ray film (Eastman Kodak).

As shown in lanes 3-5 of Figure 32, both pBG380 (rsT4.2) and pBG381 (rsT4.3) directed the synthesis of a secreted, immune, <sup>35</sup>S-labelled T4 protein that was recognized by the OKT4 anti-T4 antibody. The immunoprecipitated truncated molecules migrated as 49 Kd proteins, a result consistent with their predicted molecular weights. In contrast, no soluble T4 antigen could be detected in the conditioned media of cell lines stably transfected with pBG377 (rsT4.1) or pBG379 (rfIT4). Immunoprecipitation analysis of cellular extracts of cell lines transfected with pBG377 suggests that the rsT4.1 gene may be misfolded, which could account for a block in its secretion [M. J. Gething et al., Cell, 46, pp. 939-50 (1986)].

In Figure 32, the lanes represent the following: Lane 1: immunoprecipitation from conditioned medium of CHO cells stably co-transfected with vectors pBG312 and pAdD26. Lane 2: blank. Lanes 3 and 4: immunoprecipitation from conditioned medium of CHO cells stably co-transfected with pBG380 (rsT4.2) and pAdD26. Lanes 5 and 6: immunoprecipitation from conditioned medium of CHO cells stably

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co-transfected with pBG381 (rsT4.3) and pAdD26.  
Lane 7: immunoprecipitation from conditioned medium  
of CHO cells stably co-transfected with recombinant  
full length T4 (pBG379) and pAdD26. In Figure 32,  
5 the arrow indicates the predicted position of the  
soluble T4 from pBG380 or pBG381 relative to the  
migration of standard molecular weight markers.

Immunoprecipitation Of COS 7 Cell Lines  
Producing Recombinant Soluble T4

10 We expressed recombinant soluble T4  
derivatives pBG392, pBG393 and pBG394 in COS 7 cells  
by electroporation, essentially as described by  
G. Chu et al., "Electroporation For The Efficient  
Transfection Of Mammalian Cells With DNA", Nuc.  
15 Acids Res., 15, pp. 1311-26 (1987). More specifi-  
cally, we introduced 20 µg closed circular plasmid  
DNA and 380 µg of carrier (sonicated salmon sperm  
DNA) into  $3 \times 10^7$  COS 7 cells. The cells were  
electroporated using a Gene Pulser (Biorad) set at  
20 300 volts. Subsequently, we incubated the COS 7  
cells in Dulbecco's Modified Eagle's Medium supple-  
mented with 10% fetal calf serum for 24 hours. We  
then harvested the conditioned media, filtered it  
through a Millipore Millidisk 0.22 µ hydrophilic  
25 filter cartridge (Millipore #MCGL 305-01) and  
concentrated the secreted proteins on a fast-S ion  
exchange column (S-Sepharose Fast Flow, Pharmacia  
#17-0511-01) in 20 mM MES buffer (pH 5.5).

We then eluted the bound proteins with  
30 20 mM Tris-HCl (pH 7.7) and 0.3 M NaCl. The elution  
pool was subsequently diluted with 2 volumes of 20 mM  
Tris-HCl (pH 7.7) and it was then loaded on a column  
comprising either 19Thy anti-T4 monoclonal antibody  
and protein A Sepharose or OKT4A and protein A  
35 Sepharose. We washed the column extensively and  
eluted the bound material as 0.5 ml fractions with

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50 mM glycine-HCl (pH 2.5), 150 mM NaCl, 0.1 mM EGTA and 5 µg/ml Bovine pancreatic trypsin inhibitor, Aprotinin (Sigma, #A1153). The immunoprecipitates were subjected to SDS PAGE (10% gel) followed by immunoblotting against rabbit antisera raised against peptide JB-1. We employed silver stained gels to follow binding and elution of rsT4 during chromatography.

Figure 33 depicts an immunoblot analysis of transiently expressed pBG392 (rsT4.7) [lanes 10, 11]; pBG393 (rsT4.8) [lanes 4, 7, 8] and pBG394 (rsT4.9) [lane 5]. The standards are 50 ng purified rsT4.3 (lane 1); 150 ng purified rsT4.3 (lane 2) and 250 ng purified rsT4.3 (lane 3). The arrow indicates the expected position of migration of a protein with the relative molecular weight of rsT4.7: 21,000 daltons. The sample that was to be loaded into lane 4 was lost and lanes 6 and 9 are blank.

As shown in lanes 10 and 11 of Figure 35, pBG392 (rsT4.7) directed the synthesis of a secreted, immune protein that was recognized by the anti-T4 antibodies OKT4A and 19Thy. Lanes 4, 7 and 8 also demonstrate that pBG393 (rsT4.8) directed the synthesis of a secreted, immune protein that was recognized by OKT4A and 19Thy. This analysis illustrates that rsT4.7 contains the OKT4A epitope. It also suggests that the binding region for HIV envelope binding resides in the amino 182 terminal residues of T4.

In contrast, no soluble T4 could be detected in the media of cell lines transfected with pBG394 (rsT4.9) [see lane 5]. Immunoprecipitation analysis of cellular extracts of cell lines transfected with pBG397, however, showed that rsT4.9 was recognized by OKT4A. We believe that rsT4.9, a 113 amino acid construct, binds the HIV virus and that it represents a second generation soluble T4, one with only two

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cysteines and one of three disulfide bridges. Accordingly, rsT4.9 is easily produced in E.coli or yeast systems.

5 Similarly, although no soluble T4 could be detected in the media of cell lines transfected with pBG396 (rsT4.12), analysis of cellular extracts of those cell lines showed that rsT4.12 was recognized by OKT4A. Thus, rsT4.12 may also bind HIV virus.

10 Radioimmunoassay And Epitope Analysis Of rsT4.113

In order to determine if the 113 fragment of rsT4 contained structural determinants for binding to OKT4A, Leu-3A and OKT4, we then carried out radioimmunoassay and epitope analysis of rsT4.113  
15 using a competitive inhibition radioimmunoassay [C. J. Newby et al., "Solid-Phase Radioimmune Assays" in Handbook Of Experimental Immunology, D. M. Weir (Ed.), 1, pp. 34.1-34.8 (1986)]. As OKT4A and Leu-3A block infectivity of HIV in vitro [Dalgleish et al.,  
20 supra] and binding of T4 to gp120/160 [McDougal et al., supra], this analysis served as a first approximation as to whether or not rsT4.113 contained structural elements for interaction with HIV.

We first coated U-bottom 96 well microtiter  
25 plates (Falcon) with 50 µl/well goat-anti-mouse IgG (Byclone Typing Kit, Logan, Utah) in PBS (pH 7.0) to a concentration of 50 µg/ml and incubated the plates overnight at 4°C. We then rinsed the plates with 1X PBS and blotted them dry. The plates were then  
30 blocked by the addition of 100 µl/well of a 1X PBS solution containing 5% bovine serum albumin for 1 hour at room temperature. We rinsed the plates with PBS, blotted dry and then spotted them with 50 µl of one of three antibody solutions containing  
35 either OKT4 (10 µg/ml in block buffer); OKT4A (500 ng/ml in block buffer) or Leu-3A (Becton-

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Dickinson) (500 ng/ml in block bu-fer). We let the plates stand for 2 hours at room temperature. We then washed the plates 3 times with a PBS/0.05% Tween-80 solution and 2 times with 1X PBS and blotted them dry.

In a separate plate, we titrated competitor samples of unlabeled rsT4.113.1 from 20 µg/ml and serially diluted twice (including no competitor control), with final volumes in each well of 25 µl. The positive control for this assay was competition with unlabeled rsT4.3 (375 amino acids). We then added 25 µl of <sup>125</sup>I-rsT4.3 containing 10,000 cpm/25 µl (prepared according to A. E. Bolton and W. M. Hunter, Radioimmunoassay And Related Methods, Chapter 2c). Subsequently, we spotted the entire 50 µl content of each well onto the assay plate containing each of the three antibody solutions and incubated for 2 h at room temperature. We then washed the plates 3 times with a PBS/0.5% Tween-80 solution and 2 times with 1X PBS, blotted them dry and then counted the wells in a Beckman gamma counter for radioactivity.

As shown in Figure 34, rsT4.113.1 competes with <sup>125</sup>I-rsT4.3 for absorption to an OKT4A solid phase in a dose-dependent manner. Additionally, rsT4.113.1 competes with <sup>125</sup>I-rsT4.3 for absorption to a Leu-3A solid phase in a dose-dependent manner. By comparison to unlabeled rsT4.3, rsT4.113.1 exhibits a molar affinity for those antibodies within a factor of 3. In the 0.4 to 25 µg/ml concentration range tested, rsT4.113 did not compete with radiolabelled rsT4.3 for binding to OKT4. In a similar assay, we observed that rsT4.111 also competes with <sup>125</sup>I-rsT4.3 for binding to OKT4A and Leu-3A, but not to OKT4 [Figures 35-37].

Based on these results, we believe that the epitopes for OKT4A and Leu-3A are contained within

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the amino-terminal 113 amino acids of T4. We also believe that the epitope for OKT4 binding is localized within the carboxy terminal of the T4 polypeptide.

Accordingly, we believe that the gp120-binding domain is localized within the amino terminal 113 or 111 amino acids of the T4 protein. Based on this belief, we synthesized various synthetic oligopeptides which contain sequence within that structural domain. These oligopeptides are represented in Figure 3 as follows:

	<u>Oligopeptide</u>	<u>Amino Acid Coordinates</u>
	JB-1	44-63
	rsT4 #6	18-29
	rsT4 #7	5-56
15	rsT4 #8	84-97
	rsT4 #9	30-63

We synthesized these peptides using conventional phosphoamide DNA synthesis techniques [Tetrahedron Letters, 22, pp. 1859-62 (1981)]. We synthesized the peptides on an Applied Biosystems 380A DNA Synthesizer and purified them by gel electrophoresis.

#### ELISA Assay For rsT4.113

We also carried out an ELISA assay for rsT4.113.1 produced by p211-11-transformed E.coli. Throughout this assay, dilutions were made in blocking solution and, between each step, we washed the plates with PBS/0.05% Tween-20. More specifically, we coated wells of Immulon 2 (Dynatech, Chantilly, Virginia) plates with .005 OD (280 nm)/ml of OKT4 (IgG2b) in 0.05 M bicarbonate buffer to a volume of 50 µl/well and incubated the plates overnight at 4°C. We then blocked the plates with 5% bovine serum albumin in PBS, 200 µl/well, and incubated for 30 minutes at room temperature.

Subsequently, we added 50 µl of 50 ng/ml rsT4.3 to each well, incubating overnight at 4°C.

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We then added 50  $\mu$ l/well of a mixture containing rsT4.113.1 and 10 ng/ml of OKT4A and incubated for 2 1/2 hours at room temperature. Using a Hyclone Kit (Hyclone), we then carried out the following steps. First, we added 1 drop of rabbit anti-mouse IgG2a to each well and incubated the plates for 1 hour at room temperature. We then added 100  $\mu$ l of peroxidase-labeled anti-rabbit IgG, diluted 1:4000 with blocking buffer to each well, and incubated for 1 hour at room temperature.

We prepared a substrate reagent as follows. We diluted substrate reagent 1:10 in distilled water and added two O-phenyl-ethylene-diamine ("OPD") chromophore tablets per 10 ml of substrate. We let the mixture dissolve thoroughly by mixing with a vortex. Alternatively, a TMB peroxidase substrate system (Kirkegaard & Perry Catalogue #50-76-00) may be used. Subsequently, we added 100  $\mu$ l of the chromophore solution to each well, incubated for 10-15 minutes at room temperature and then stopped the color development with 100  $\mu$ l of 1N  $H_2SO_4$ . We then measured OD at 490 nm, using an ELISA plate reader.

The results of the assay are demonstrated in Figure 38.

We then subjected the soluble T4 proteins produced by the T4 constructs of this invention to various functional assays.

#### Assays Of The Antiviral Activity Of Soluble T4

The antiviral activity of soluble T4 according to this invention was evaluated using modifications of various in vitro systems used to study antiviral agents and neutralizing antibodies [D. D. Ho et al., "Recombinant Human Interferon Alpha (A) Suppresses HTLV-III Replication In Vitro", Lancet, pp. 602-04 (1985); K. Hartshorn et al.,

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"Synergistic Inhibition Of HTLV-III Replication  
In Vitro By Phosphonoformate And Recombinant Inter-  
feron Alpha-A", Antimicrob Ag Chemoth. 30, pp. 189-91  
(1986)].

5           For each of these assays, we prepared graded  
concentrations of soluble T4 and preincubated them  
with an H9 derived IIIB isolate of HIV [a gift from  
Drs. M. Popovic and R. Gallo, National Cancer  
Institute, Bethesda, Maryland]. The isolate was  
10 maintained as a chronically infected culture in H9  
cells. Cell-free HIV stocks were obtained from  
supernatant fluids of HTLV-III infected H9 cultures  
(culture conditions:  $1 \times 10^6$  cells/ml with 75% viable  
cells). We prepared serial 10 fold dilutions of  
15 recombinant soluble T4 ranging from 10 picograms/ml  
to 10 micrograms/ml and incubated them with fifty  
50% tissue culture infectious doses (TCID<sub>50</sub>) of HIV  
for 1 hour at 37°C, in RPMI-1640 supplemented with  
20% heat inactivated fetal calf serum (FCS). We  
20 then added 150 µl of H9 cells to a final concentra-  
tion of  $0.5 \times 10^6$  cells/ml which were not HIV-infected  
to the wells containing aliquots of the recombinant  
soluble T4/HIV mixture.

We adjusted each virus inoculum to a con-  
25 centration of 250 TCID<sub>50</sub>/ml. We preincubated 100 µl  
of the virus inoculum with 200 µl recombinant solu-  
ble T4 or 100 µl immunoglobulin prepared in tripli-  
cate serial 2-fold dilutions for 1 hour at 37°C  
prior to inoculation onto  $1.5 - 2 \times 10^6$  H9 cells in  
30 5 ml RPMI 1640 supplemented fetal calf serum (20%),  
HEPES (10mM), penicillin (250 U/ml), streptomycin  
(250 µg/ml) and L-glutamine (2mM). On days 5, 6, 7,  
10 and 14, we examined each culture for characteris-  
ic cytopathic effects ("CPE"). Neutralization was  
35 defined as the inhibition of syncytia formation com-  
ared with controls.

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The positive control used was HIV seropositive neutralizing serum, as described in D. D. Ho et al., "Human Immunodeficiency Virus Neutralizing Antibodies Recognize Several Conserved Domains On The Envelope Glycoproteins", J. Virol., 61, pp. 2024-28 (1987). The negative controls used were HIV seronegative serum only and buffer only.

#### Cytopathic Effect Assay (CPE)

In this assay, following conventional protocols for cytopathic effect assays [Klatzmann et al. (1984), supra and Wong-Staal and Gallo (1985), supra], we microscopically examined the H9 cells for evidence of cytopathic effects of HIV.

The CPE was scored on a four point scale from 1+ to 4+, with 4+ representing the highest degree of CPE.

By day 14, wells containing recombinant soluble T4 according to this invention (rsT4.2, derived from the pBG380 transfected CHO cell line BG380) at 10 µg/ml showed no evidence of CPE, while the negative control showed 1+ to 3+ CPE.

#### p24 Radioimmunoassay

We then tested soluble T4 as an inhibitor of viral replication in an HIV virus replication assay according to D. D. Ho et al., J. Virol., 61, pp. 2024-28 (1987) and J. Sodroski et al., Nature, 322, pp. 470-74 (1986). We carried out the assay essentially as described, except that the cultures were propagated in microtiter wells containing 200 µl. In this assay, we evaluated the ability of the soluble T4 polypeptides of this invention to block HIV replication, as measured by HIV p24 antigen production. We sampled supernatants twice weekly for HIV p24 antigen as described below.

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We obtained an assay kit [HTLV-III p24 Radioimmunoassay System, Catalogue No. NEK-040, NEK-040A, Biotechnology Systems, New Research Products, Dupont] which contains affinity purified  $^{125}\text{I}$  labelled HIV p24 antigen, a rabbit anti-p24 antibody and a second goat anti-rabbit antibody which is used to precipitate antigen-antibody complexes. We carried out the assay according to the protocol included with the kit. Accordingly, we mixed a sample to be assayed or one of a series of amounts of unlabelled p24 antigen with a fixed amount of  $^{125}\text{I}$  labelled p24 and a fixed limited amount of rabbit anti-p24 antibody. We incubated the samples overnight at room temperature and then added a goat anti-rabbit immunoglobulin preparation for 5 minutes at  $40^\circ\text{C}$ . We centrifuged the samples in a microfuge and aspirated the supernatant fluid. Pelleted  $^{125}\text{I}$  labelled p24 was quantitated for each sample by gamma counting and a standard curve for the  $^{125}\text{I}$  p24 displaced by the known amounts of antigen added to standard tubes was constructed. We then calculated the  $^{125}\text{I}$  labelled p24 displaced by the antigen present in the unknown samples by interpolation using the standard curve constructed from the known amounts of p24 antigen contained in the standard samples. The results are shown in the table below.

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p24 ASSAY OF HIV REPLICATION INHIBITION

	Day	rsT4.2 ( $\mu$ g/ml)	Patient Serum	Average CPM	% Bound/ Unbound
5	7	-	Negative	344	8.5
		-	Positive	2,237	112.4
		0.5*	-	551	19.9
		5.0**	-	1,766	86.6
10	10	-	Negative	230	2.2
		-	Positive	2,459	124.6
		0.5*	-	322	7.3
		5.0**	-	1,980	96.3
15	14	-	Negative	221	1.8
		-	Positive	2,284	115.0
		0.5*	-	246	3.1
		5.0**	-	1,988	98.7

These results demonstrate that soluble T4 according to this invention at a concentration of 5  $\mu$ g/ml completely inhibits virus replication as measured in this standard 14 day assay. These results are also depicted in Figure 39 in graphic form. In Figure 39, values were calculated from a standard curve of p24 according to assay kit instructions.

\* This concentration was initially believed to be 1.0  $\mu$ g/ml, based upon our preliminary approximation that 1 unit of absorbance at 280 nm (" $A_{280}$ "), was equivalent to 1 mg of rsT4.2. Absorbance at 280 nm is a commonly used first approximation of protein concentration. Upon amino acid analysis of the protein, however, we found that it had a higher extinction coefficient than originally approximated, with 1  $A_{280}$  unit of rsT4.2 being equivalent to 0.5 mg of the protein.

\*\* This concentration was initially believed to be 10  $\mu$ g/ml, based upon our preliminary approximation that 1 unit of absorbance at 280 nm (" $A_{280}$ "), was equivalent to 1 mg of rsT4.2. Absorbance at 280 nm is a commonly used first approximation of protein concentration. Upon amino acid analysis of the protein, however, we found that it had a higher extinction coefficient than originally approximated, with 1  $A_{280}$  unit of rsT4.2 being equivalent to 0.5 mg of the protein.

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We then carried out a p24 replication assay as described above, except that the soluble T4 was added to the infected cultures during refeeding at days 3, 7 and 10, in order to maintain a constant rsT4 concentration throughout the infection period. The results of this assay are shown in the table below.

INHIBITION OF HIV REPLICATION  
WITH CONSTANT CONCENTRATION OF rsT4

	rsT4.2 ( $\mu\text{g/ml}$ )	p24 (ng/ml)
10	0.008	770
	0.031	970
	0.125	85
15	0.5	0
	5.0	0
	0	1120
	uninfected	0

These results demonstrate that when soluble T4 protein according to this invention was maintained at a constant concentration throughout the infection period, as little as 0.125  $\mu\text{g/ml}$  of the protein substantially blocked replication of 250 TCID<sub>50</sub>/ml of HIV-1.

Advantageously, soluble T4 protein according to this invention, at concentrations far exceeding those required to block viral replication, did not exert immunotoxic effects in vitro, as measured by three lymphocyte proliferation assays -- mixed lymphocyte response, phytohemagglutinin, and tetanus toxoid stimulated response.

Syncytia Inhibition Assay

To further assess the effect of soluble T4 on HIV env-T4 binding, we evaluated the effect of two preparations of our soluble T4 protein on the syncytiagenic properties of HIV in the co-cultivation assay. We carried out a C8166 cell fusion assay

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as described in B. D. Walker et al., Proc. Natl. Acad. Sci. USA, 84, pp. 8120-24 (1987).

We incubated  $1 \times 10^9$  H9 cells chronically infected with HTLV-IIIB for 1 hour at 37°C in 5% CO<sub>2</sub> with various concentrations of one of two preparations of rsT4.2 in 150 µl RPMI-1640 media supplemented with 20% fetal calf serum. We then added  $3 \times 10^4$  C8166 cells in 50 µl media (a T4<sup>+</sup> transformed human umbilical cord blood lymphocyte line [Sodroski et al., supra], to a final volume of 0.2 ml in each well. Final well concentrations of soluble T4 were 0.5 µg/ml\* and 5.0 µg/ml\* for preparation #1 and 1.25 µg/ml\* and 12.5 µg/ml\* for preparation #2. We then counted total number of syncytia per well at 2 hours and 4 hours after adding the C8166 cells at 37°C in 5% CO<sub>2</sub>. Parallel co-cultivations used buffer alone (negative control) or OKT4A at 25 µg/ml (positive control) as controls. We considered a positive result as a 50% reduction in syncytia compared to controls, at a time when at least 100 syncytia per  $10^4$  infected H9 cells were present in the control cultivations. The results of this assay are shown below and in Figure 40 (2 hour data).

25

\* These concentrations were initially believed to be, respectively, 1 µg/ml, 10 µg/ml, 2.5 µg/ml and 25 µg/ml, based upon our preliminary approximation that 1 unit of absorbance at 280 nm ("A<sub>280</sub>"), was equivalent to 1 mg of rsT4.2. Upon amino acid analysis of the protein, however, we found that it had a higher extinction coefficient than originally approximated, with 1 A<sub>280</sub> unit of rsT4.2 being equivalent to 0.5 mg of the protein.

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INHIBITION IN C8166 FUSION ASSAY

	<u>Preparation</u>	<u>[rsT4.2] (<math>\mu\text{g/ml}</math>)</u>	<u>% Inhibition*</u>	
			<u>2 Hrs</u>	<u>4 Hrs</u>
	buffer	0	0	0
5	rsT4.2	0.5**	30	42
	rsT4.2	5.0**	54	47
	rsT4.2	1.25**	16	21
	rsT4.2	12.5**	77	55
	OKT4A (25 $\mu\text{g/ml}$ )	0	100	100

10                   As demonstrated in this table and in Figure 40, soluble T4 according to this invention at 5.0  $\mu\text{g/ml}$  and 12.5  $\mu\text{g/ml}$  inhibited syncytia formation at 2 hours, as compared to buffer alone. By 4 hours after the addition of C8166 cells, soluble T4 at 12.5  $\mu\text{g/ml}$  continued to inhibit greater than 50% syncytia formation, as compared to the negative control.

15                   We also evaluated the effect of two preparations of our soluble T4 protein rsT4.7 on the syncytiagenic properties of HIV in a similar co-cultivation assay. The results of this assay are shown below.

25                   \* All assays were carried out in triplicate, and the number of syncytia counted per well was averaged to calculate % inhibition. The % inhibition represents the difference between the average number of syncytia in the negative control (without rsT4 or OKT4A) and the average number of syncytia counted when either rsT4 or OKT4A were present during the assay, divided by the average syncytia count for the negative control and multiplied by 100.

30                   \*\* These concentrations were initially believed to be, respectively, 1  $\mu\text{g/ml}$ , 10  $\mu\text{g/ml}$ , 2.5  $\mu\text{g/ml}$  and 25  $\mu\text{g/ml}$ , based upon our preliminary approximation that 1 unit of absorbance at 280 nm (" $A_{280}$ "), was equivalent to 1 mg of rsT4.2. Upon amino acid analysis of the protein however, we found that it had a higher extinction coefficient than originally approximated, with 1  $A_{280}$  unit of rsT4.2 being equivalent to 0.5 mg of the protein.

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INHIBITION IN C8166 FUSION ASSAYAssay date: day 1

	<u>Preparation</u>	<u>rsT4.7 (<math>\mu\text{g/ml}</math>)</u>	<u>Average Syncytia/50<math>\mu\text{l}</math> aliquot</u>	<u>% Inhibition at 2 Hrs</u>
5	H9 cells (control)	0	0	N/A
	C8166 cells (control)	0	0	N/A
10	HIV-infected H9 cells added to C8166 cells (control)	0	118	0
15	OKT4A (control)	0	0	100
	Prep. 1 of rsT4.7	$\approx 5.0^*$	43	63.6

- 20 \* This concentration was initially believed to be 10  $\mu\text{g/ml}$ , based upon our preliminary approximation that 1 unit of absorbance at 280 nm (" $A_{280}$ "), was equivalent to 1 mg of rsT4.2. Upon amino acid analysis of the protein, however, we found that it
- 25 had a higher extinction coefficient than originally approximated, with 1  $A_{280}$  unit of rsT4.2 being equivalent to 0.5 mg of the protein.

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Assay date: day 13

	<u>Preparation</u>	<u>rsT4.7 (<math>\mu</math>g/ml)</u>	<u>Average Syncytia/50<math>\mu</math>l aliquot</u>	<u>% Inhibition at 2 Hrs</u>
5	H9 cells (control)	0	0	N/A
	C8166 cells (control)	0	1	N/A
10	HIV-infected H9 cells added to C8166 cells (control)	0	141	0
	OKT4A (control)	0	0	100
15	Prep. 2 of rsT4.7	$\approx$ 5.0*	27	80.9

\* This concentration was initially believed to be 10  $\mu$ g/ml, based upon our preliminary approximation that 1 unit of absorbance at 280 nm (" $A_{280}$ "), was equivalent to 1 mg of rsT4.2. Upon amino acid analysis of the protein, however, we found that it had a higher extinction coefficient than originally approximated, with 1  $A_{280}$  unit of rsT4.2 being equivalent to 0.5 mg of the protein.

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Assay date: day 14

	<u>Preparation</u>	<u>rsT4.7 (µg/ml)</u>	<u>Average Syncytia/50µl aliquot</u>	<u>% Inhibition at 2 Hrs</u>
5	H9 cells (control)	0	0	N/A
	C8166 cells (control)	0	0	N/A
10	HIV-infected H9 cells added C8166 cells (control)	0	128	0
	OKT4A (control)	0	0	100
15	Prep. 1 of rsT4.7	≅ 5.0*	35	72.7
	Prep. 2 of rsT4.7	≅ 5.0*	2	98.4

As demonstrated in these tables, soluble T4 protein rsT4.7 inhibited syncytia formation in HIV-infected H9 cells.

We also evaluated the effect of rsT4.113.1 and rsT4.111 on the syncytiogenic properties of HIV in a co-cultivation assay. We carried out a C8166 cell fusion assay as described in Walker et al., supra.

We incubated  $1 \times 10^4$  H9 cells chronically infected with HTLV-IIIB for 1 hour at 37°C in 5% CO<sub>2</sub>, with from 5 to 50 µg/ml rsT4.113.1 or rsT4.111 in 150 µl RPMI-1640 media supplemented with 20% fetal calf serum in 96-well microtiter plates. We

\* This concentration was initially believed to be 10 µg/ml, based upon our preliminary approximation that 1 unit of absorbance at 280 nm ("A<sub>280</sub>"), was equivalent to 1 mg of rsT4.2. Upon amino acid analysis of the protein, however, we found that it had a higher extinction coefficient than originally approximated, with 1 A<sub>280</sub> unit of rsT4.2 being equivalent to 0.5 mg of the protein.

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then added  $3 \times 10^4$  C8166 cells to the wells in 50  $\mu$ l aliquots. The plates were incubated for 2 hours at 37°C in 5% CO<sub>2</sub> and, following this incubation, the number of syncytia per well were counted.

- 5 Syncytia were defined as cells containing a ballooning cytoplasm greater than three cell diameters. All samples were counted twice. Parallel co-cultivation used OKT4A alone or rsT4.3 alone at a concentration of 25  $\mu$ g/ml (positive controls) or H9  
10 cells alone or C8166 cells alone (negative controls). The results of this assay are shown below and in Figure 41.

#### INHIBITION IN C8166 FUSION ASSAY

	<u>Preparation</u>	<u>rsT4(<math>\mu</math>g/ml)</u>	<u>% Inhibition</u>
15	H9 cells (control)	0	0
	C8166 cells (control)	0	0
	rsT4.113.1	1.25	35
	rsT4.113.1	2.5	63
	rsT4.113.1	4.25	63
20	rsT4.113.1	6.25	82
	rsT4.113.1	12.5	96
	rsT4.3	12.5	100
	OKT4A (25 $\mu$ g/ml)	0	100

- As demonstrated in this table and in  
25 Figure 41, rsT4.113.1 exhibited a dose-dependent inhibition of HIV-induced syncytia formation. The molar specific inhibitory activity of rsT4.113.1 appeared to be reduced by an order of magnitude by comparison to anti-viral activity of longer forms of  
30 recombinant soluble T4. Thus, whereas rsT4.113.1 is effective toward neutralization of HIV-dependent cell fusion in vitro, its molar specific inhibitory

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activity is decreased by a factor of 10. It is undetermined whether this decreased potency is due to incomplete renaturation of the E.coli-derived protein, the presence of three additional amino acids at the N-terminus of rsT4.113.1 (Met-Gln-Gly) lacking in rsT4.2 or rsT4.3 produced in mammalian cells, or the absence of additional structure in rsT4.113.1 required for high-affinity binding to HIV.

We also carried out a C8166 cell fusion assay with rsT4.111, as described for rsT4.113.1. The results of this assay are shown below.

#### INHIBITION IN C8166 FUSION ASSAY

	<u>Preparation</u>	<u>rsT4(µg/ml)</u>	<u>% Inhibition</u>
15	H9 cell (control)	0	0
	C8166 cells (control)	0	0
-	rsT4.111	1.25	0
	rsT4.111	2.5	40
	rsT4.111	4.25	20
	rsT4.111	6.25	67
20	rsT4.111	12.5	100
	rsT4.111	25.0	100
	rsT4.3	12.5	100
	rsT4.3	25.0	100
25	OKT4A (25 µg/ml)	0	100

As demonstrated in this table, rsT4.111 exhibited a dose-dependent inhibition of HIV-induced syncytia formation. At a concentration of 12.5 µg/ml and 25.0 µg/ml, complete inhibition of cell fusion was achieved.

#### Kinetics Of Intramuscular Injection Of Soluble T4

We examined the kinetics of the appearance of a recombinant soluble T4 protein according to this invention (specifically, rsT4.3 from the pBG381-transfected cell line BG381) in serum after intramuscular injection as follows.

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We obtained two cynomolgus monkeys (Macaca fascicularis) who were free of infectious disease and in good health. Each monkey had been subjected to a 6 week quarantine period prior to administration of the soluble T4 protein. Throughout the administration period, each monkey was maintained on a conventional diet of monkey chow supplemented with fresh fruit. A catheter and a vascular access port were surgically placed in a femoral vein of each animal prior to treatment in order to facilitate blood collection.

Over a period of 28 days, each animal received recombinant soluble T4 protein twice daily by intramuscular injection to the large muscles of the thighs or buttocks. Injections were administered to each animal 8 hours apart and each injection contained a volume of 0.15 ml/kg (0.25 mg/kg) of rsT4.3 (from the pBG381-transformed cell line BG381), for a total dose of 0.5 mg/kg/day/monkey. Serum samples for clearance determination were collected on day 1 before the first treatment and at 1, 2, 4 and 8 hours after the first injection, as well as 1, 2, 4, 14 and 16 hours after the second injection on days 7, 14 and 28.

We found that intramuscularly injected soluble T4 reached the maximum level in serum between 1 and 2 hours after injection, with the level falling off slowly and reaching half-maximum value at approximately 6 hours post-injection. According to data obtained for intravenous administration (not shown), the level of rsT4.3 in serum should drop below that attained via intramuscular injection approximately 2 hours after intravenous injection. Thus, while the maximum rsT4.3 level in serum after intramuscular injection does not reach that attainable via intravenous injection, it is slowly released into the blood stream, remaining detectable in serum for a

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much longer time. This slow release mechanism associated with intramuscular routes of injection is advantageous because a higher level of soluble T4 protein is available over a longer period of time over a given concentration; thus remaining in a sustained level. Intramuscular administration of soluble T4 protein is particularly useful in treating early stage HIV-infected patients, to prevent the virus from disseminating, or in treating patients who have been exposed to the virus and who are not yet seropositive.

We determined serum levels of rsT4.3 using an ELISA assay. Throughout this assay, dilutions were made in blocking solution and, between each step, we washed the plates with PBS/0.05% Tween-20. More specifically, we coated wells of Immulon 2 plates with .01 OD (280 nm)/ml of OKT4 (IgG2b) in 0.05 M bicarbonate buffer to a volume of 50 µl/well and incubated the plates overnight at 4°C. We then blocked the plates with 5% bovine serum albumin in PBS, 200 µl/well, and incubated for 30 minutes at room temperature.

Subsequently, we added 50 µl of sample or standard to each well, incubating for 4 hours at room temperature. We then added 50 µl/well of OKT4A at 0.1 µg/ml and incubated overnight at 4°C. Using a Byclone Kit (Byclone) we then carried out the following steps. First, we added 1 drop of rabbit anti-mouse IgG2a to each well and incubated the plates for 1 hour at room temperature. We then added 100 µl of peroxidase-labeled anti-rabbit IgG, diluted 1:4000 with 5% BSA/PBS to each well, and incubated for 1 hour at room temperature.

We prepared a substrate reagent as follows. We diluted substrate reagent 1:10 in distilled water and added two O-phenyl-ethylene-diamine ("OPD") chromophore tablets per 10 ml of substrate. We let

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the mixture dissolve thoroughl: by mixing with a vortex. Alternatively, a TMB peroxidase substrate system (Kirkegaard & Perry Catalogue #50-76-00) may be used. Subsequently, we added 100  $\mu$ l of the

5 chromophore solution to each well, incubated for 10-15 minutes at room temperature and then stopped the color development with 100  $\mu$ l of 1N  $H_2SO_4$ . We then measured OD at 490 nm, using an ELISA plate reader.

10 The results of the assay are demonstrated in the tables below.

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Monkey #7-91

		<u>rsT4 Level</u> <u>(ng/ml)</u>			
	<u>Time(hr)</u>	<u>Day 1</u>	<u>Day 7</u>	<u>Day 14</u>	<u>Day 28</u>
5	0	22.7*	96.5	158.0	19.8
	1	278.8	199.6	360.7	238.3
	2	281.8	366.8	306.4	441.1
	4	214.9	246.6	363.9	393.2
	5				290.4
10	8	72.3	105.0	199.4	
	9**	246.2			
	10	259.6			
	12	136.0			
	22	23.8			
15	24	13.4			

Monkey #7-92

		<u>rsT4 Level</u> <u>(ng/ml)</u>			
	<u>Time(hr)</u>	<u>Day 1</u>	<u>Day 7</u>	<u>Day 14</u>	<u>Day 28</u>
20	0	6.7*	56.0	106.3	60.9
	1	87.2	225.8	178.0	437.7
	2	254.2	377.9	253.2	770.6
	4	170.0	167.3	308.2	821.5
	5				898.3
25	8	118.9	101.2	176.5	
	9**	405.1			
	10	523.5			
	12	371.5			
	22	48.4			
30	24	39.4			

\* - background

\*\* - second injection administered after the collection of the 8 hour sample.

Polyvalent Forms Of Recombinant Soluble T4

35            Receptors may be characterized by their affinity for specific ligands, such that, at equilibrium, the intrinsic affinity ( $K_a$ ) between monovalent receptor and monovalent ligand can be defined as

40             $[RL]/[R_f][L_f]$ , where  $[RL]$  is the concentration of receptor (R) bound to ligand (L) and  $[R_f]$  and  $[L_f]$  are the concentrations of free receptor and ligand,

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respectively [P. A. Underwood, in Advances In Virus Research, ed. K. Maramorosch et al., 34, pp. 283-309 (1988)].

For a polyvalent receptor (with a valency of  $n$ ) binding to a polyvalent ligand (with a valency of  $m$ ), a functional affinity can be defined as  $n[R_b]/n[R_f]m[L_f]$ , where  $[R_b]$  is the concentration of bound receptor sites, and  $n[R_f]$  and  $m[L_f]$  are, respectively, the concentrations of free receptor and ligand binding sites. The effect of increasing the valence (the number of binding sites) is to enhance the stability of ligand-receptor complexes. The affinity of a polyvalent receptor for a polyvalent ligand will depend on three factors: the intrinsic association constant of each binding site, the valency (number of binding sites) and the topological relationship between the receptor and ligand binding sites. Under some circumstances, polyvalent binding interactions will lead to higher functional affinity. The decreased dissociation rate of polyvalent ligands with polyvalent receptors results in an increased functional affinity [C. L. Hornick and F. Karush, Immunochemistry, 9, pp. 325-40 (1972); I. Otterness and F. Karush, "Principles Of Antibody Reactions", in Antibody As A Tool, ed. J. J. Marchalonis and G.W. Warr, pp. 97-137 (1982)].

The simplest case for receptor polyvalency increasing functional affinity is represented by a bivalent soluble receptor, such as an antibody molecule, which has two identical ligand binding sites, each capable of independently binding antigen with equal affinity. If the antigen is displayed polyvalently, for example, chemically coupled to a solid support such that the spacing between antigenic sites can be bridged by the antibody's two antigen binding arms, the functional affinity of the antibody for the antigen coupled to the solid support would be



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greater than the intrinsic affinity of the antibody binding site for the monovalent antigen [D. Crothers and H. Metzger, Immunochemistry, 9, pp. 341-57 (1972)]. Because virus particles represent polyvalent antigens, the greater functional affinity of antibodies for polyvalent antigens is an important factor for antibody-directed virus neutralization.

The association of recombinant soluble T4 and the HIV major envelope glycoprotein gp120 is an example of monovalent receptor binding to monovalent ligand. The affinity of this interaction has been measured, and the association between T4 and gp120 has a dissociation constant  $K_d = 4 \times 10^{-9}$  M [L. Lasky et al., Cell, 50, pp. 975-88 (1987)].

Using the antibody analogy, we believe that polyvalent rsT4 will demonstrate a greater affinity for HIV-infected cells displaying gp120 than monovalent rsT4 and the topological relationship between gp120 on the virus particle or the infected cell surface, will determine the degree to which polyvalent rsT4 exhibits higher functional affinity than monovalent rsT4. One example of a polyvalent rsT4 is described below, with respect to the production of a recombinant bivalent rsT4 consisting of two tandem repeats of amino acids 3-178, followed by the C-terminal 199 amino acids of rsT4.3. According to this invention, a "polyvalent" receptor possesses two or more binding sites for a given ligand. Furthermore, the intrinsic affinity of each ligand binding site of a given polyvalent receptor need not be identical.

As shown in Figure 42, to construct bivalent rsT4, we digested pBG391 with NheI, which cleaves after the valine at position 178 in rsT4, and removed the NheI 5' overhang with mung bean nuclease. Next, we cleaved with BglII to remove the C-terminal half of the rsT4 coding sequence in pBG391. Finally, we

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ligated a DraI-BglII fragment containing the coding sequence for rsT4 amino acids 3 (lysine) through 377 (isoleucine) to the cleaved pBG391 to create pBiv.1, a plasmid coding for a fusion protein with a tandem duplication of the N-terminal 176 amino acids of rsT4, followed by the C-terminal 199 amino acids of rsT4.3. The protein produced by this plasmid, therefore, contains two adjacent N-terminal gp120-binding or OKT4A-binding domains (defined by amino acid residues 3 through 111 of rsT4.111), followed by one OKT4-binding C-terminal domain (Figure 43).

pBiv.1 was transfected by electroporation into COS 7 cells to test expression of the bivalent rsT4 protein. Three days later, we tested the conditioned medium of the transfected cells for the presence of the rsT4 bivalent protein by immunoprecipitation, followed by Western blot analysis of the precipitated protein. Both OKT4A and OKT4 were used for immuno-precipitation to determine that the OKT4 epitope and at least one of the OKT4A epitopes had folded correctly. Both antibodies precipitated a protein of the predicted apparent molecular weight (60,000d) from the conditioned medium of the cells.

Bivalent rsT4 may be purified by immuno-affinity purification from an OKT4 column and the purified protein may then be used to perform quantitative competition assays with rsT4.3. We believe that the bivalent molecule would demonstrate equivalent competition against rsT4.3 for OKT4 binding, but significantly greater competition against monovalent rsT4 for OKT4A binding. The ability of bivalent recombinant soluble T4 to block syncytium formation may also be demonstrated in the C8166 fusion assay. We also believe that bivalent recombinant soluble T4 would block syncytium formation at significantly lower concentrations than monovalent rsT4; based upon the higher

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functional affinity of bivalent recombinant soluble T4 for gp120.

According to alternate embodiments of this invention, other methods for producing polyvalent rsT4 may be employed. For example, polyvalent rsT4 may be produced by chemically coupling rsT4 to any clinically acceptable carrier molecule, a polymer selected from the group consisting of Ficoll, polyethylene glycol or dextran, using conventional coupling techniques. Alternatively, rsT4 may be chemically coupled to biotin, and the biotin-rsT4 conjugate then allowed to bind to avidin, resulting in tetravalent avidin/biotin/rsT4 molecules. And rsT4 may be covalently coupled to dinitrophenol (DNP) or trinitrophenol (TNP) and the resulting conjugate precipitated with anti-DNP or anti-TNP-Igm, to form decameric conjugates with a valency of 10 for rsT4 binding sites.

Alternatively, a recombinant chimeric antibody molecule with rsT4 sequences substituted for the variable domains of either or both of the immunoglobulin molecule heavy and light chains may be produced. Because recombinant soluble T4 possesses gp120 binding activity, the construction of a chimeric antibody having two soluble T4 domains and having unmodified constant region domains could serve as a mediator of targeted killing of HIV-infected cells that express gp120.

For example, chimeric rsT4/IgG<sub>1</sub> may be produced from two chimeric genes -- an rsT4/human kappa light chain chimera (rsT4/C<sub>kappa</sub>) and an rsT4/human gamma 1 heavy chain chimera (rsT4/C<sub>gamma-1</sub>). Both C<sub>kappa</sub> and C<sub>gamma-1</sub> regions have been isolated from human recombinant DNA libraries, and each has been subcloned into animal cell selection vectors containing either the bacterial neo resistance or bacterial gpt markers

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for selection in animal cell hosts against the antibiotic G418 or mycophenolic acid, respectively.

To construct rsT4/C<sub>gamma-1</sub> and rsT4/C<sub>kappa</sub> chimeric genes, an rsT4 gene segment, including at least the secretory signal sequence and the N-terminal 110 amino acid residues of the mature rsT4 coding sequence and including a splice donor or portion thereof, is placed upstream of the gamma-1 and kappa constant domain exons. A suitable restriction enzyme may be used to cut within the intron downstream of the desired rsT4 coding sequence, thus providing a donor splice site. Subsequently, a suitable restriction enzyme is used to cut within the introns upstream of the kappa and gamma-1 coding regions. The rsT4 sequence is then joined to the kappa or gamma-1 constant region sequence, such that the rsT4 intron sequence is contiguous with the gamma-1 and kappa introns. In this way, an acceptor splice site is provided by the kappa or gamma-1 constant region intron. Alternatively, rsT4 chimeric genes may be constructed without the use of introns, by fusing a suitable rsT4 cDNA gene segment directly to the gamma-1 or kappa coding regions.

The rsT4/C<sub>gamma-1</sub> and rsT4/C<sub>kappa</sub> vectors may then be cotransfected, for example, by electroporation into lymphoid or non-lymphoid host cells. Following transcription and translation of the two chimeric genes, the gene products may assemble into chimeric antibody molecules.

Expression of the chimeric gene products may be measured by an enzyme-linked immunoadsorbant assay (ELISA) that utilizes monoclonal anti-T4 antibody OKT4A, as described infra, or in gp120 competition assays and radioimmunoassays, as described infra. Activity of the rsT4/IgG<sub>1</sub> chimeras may be measured by incubating them with HIV-infected cells in the presence of human complement, followed by quantitating

subsequent complement-mediated lysis of these cells. Alternatively, activity may be measured in HIV replication and HIV syncytium assays as described infra.

5 In order to determine if bivalent rsT4 has a greater potency than monovalent rsT4, we mixed OKT4, at various concentrations, together with a constant concentration of rsT4, so that the molar ratio of OKT4:rsT4 varied between 0.2 and 4. After preincubating the mixture overnight at 4°C, we added  
10 aliquots to the HIV syncytium assay described infra. OKT4 has no observable effect in this assay when used alone. In addition, the concentration of recombinant soluble T4 chosen did not cause inhibition in this assay. Accordingly, we looked for indications that  
15 the OKT4/rsT4 mixture was more potent than rsT4 alone. We observed that at ratios of OKT4:rsT4 greater than 0.2, partial to complete inhibition of syncytium formation occurred. We believe that under conditions where two rsT4 molecules are bound to 1 OKT4 molecule,  
20 the greatest inhibitory effect should be found.

Thus, polyvalent, as well as monovalent forms of recombinant soluble T4 are useful in the compositions and methods of this invention.

25 Microorganisms and recombinant DNA molecules prepared by the processes of this invention are exemplified by cultures deposited in the In Vitro International, Inc. culture collection, in Linthicum, Maryland, on September 2, 1987, and identified as:

30 BG378: E.coli MC1061/pBG378  
199-7: E.coli MC1061/p199-7  
170-2: E.coli JA221/p170-2  
EC100: E.coli JM83/pEC100  
BG377: E.coli MC1061/pBG377  
BG380: E.coli MC1061/pBG380  
35 BG381: E.coli MC1061/pBG381

These cultures were assigned accession  
3745 numbers IVI 10143-10149, respectively.

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In addition, microorganisms and recombinant DNA molecules according to this invention are exemplified by cultures deposited in the In Vitro International, Inc. culture collection, in Linthicum,

5 Maryland, on January 6, 1988, and identified as:

BG-391: E.coli MC1061/pBG391

BG-392: E.coli MC1061/pBG392

BG-393: E.coli MC1061/pBG393

BG-394: E.coli MC1061/pBG394

10 BG-396: E.coli MC1061/pBG396

203-5 : E.coli SG936/p203-5.

These cultures were assigned accession numbers IVI 10151-10156, respectively.

15 Microorganisms and recombinant DNA molecules according to this invention are also exemplified by cultures deposited in the In Vitro International, Inc. culture collection, in Linthicum, Maryland, on August 24, 1988 and identified as:

211-11: E.coli A89/pBG211-11

20 214-10: E.coli A89/pBG214-10

215-7 : E.coli A89/pBG215-7

These cultures were assigned accession numbers IVI 10183-10185 respectively.

25 While we have hereinbefore described a number of embodiments of this invention, it is apparent that our basic constructions can be altered to provide other embodiments which utilize the processes and compositions of this invention. Therefore, it will be appreciated that the scope of this  
30 invention is to be defined by the claims appended hereto rather than by the specific embodiments which have been presented hereinbefore by way of example.

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CLAIMS

We claim:

1. A DNA sequence selected from the group consisting of:
  - 5 (a) the DNA inserts of p199-7, pBG377, pBG380, pBG381, p203-5, pBG391, pBG392, pBG393, pBG394, pBG395, pBG396, pBG397, p211-11, p214-10 and p215-7;
  - (b) DNA sequences which hybridize to one or more of the foregoing DNA inserts and which  
10 code on expression for a soluble T4-like polypeptide; and
  - (c) DNA sequences which code on expression for a soluble T4-like polypeptide coded for on expression by any of the foregoing DNA inserts  
15 and sequences.
2. The DNA sequence according to claim 1, wherein said DNA sequence (b) codes on expression for a soluble T4-like polypeptide which inhibits adhesion between T4<sup>+</sup> lymphocytes and infective agents  
20 which target T4<sup>+</sup> lymphocytes and which inhibits interaction between T4<sup>+</sup> lymphocytes and antigen presenting cells and targets of T4<sup>+</sup> lymphocyte mediated killing.
3. A recombinant DNA molecule comprising  
25 a DNA sequence selected from the group consisting of the DNA sequences of claim 1 or 2, said DNA sequence being operatively linked to an expression control sequence in said recombinant DNA molecule.
4. The recombinant DNA molecule according  
30 to claim 3, wherein said expression control sequence is selected from the group consisting of the early or late promoters of SV40 or adenovirus, the lac system, the trp system, the TAC system, the TRC

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system, the major operator and promoter regions of phage  $\lambda$ , the control regions of fd coat protein, the promoter for 3-phosphoglycerate kinase or other glycolytic enzymes, the promoters of acid phosphatase, the polyhedron promoter of the baculovirus system and the promoters of the yeast  $\alpha$ -mating factors.

5. A unicellular host transformed with a recombinant DNA molecule selected from the group consisting of the recombinant DNA molecules of claim 3 or 4.

6. The host according to claim 5, wherein said host is selected from the group consisting of strains of E.coli, Pseudomonas, Bacillus, Streptomyces, fungi, animal cells, plant cells, insect cells and human cells in tissue culture.

7. A polypeptide coded for on expression by a DNA sequence selected from the group consisting of the DNA sequences of claim 1 or 2, said polypeptide being essentially free of other proteins of human origin.

8. The polypeptide according to claim 7, wherein said polypeptide is selected from the group consisting of a polypeptide of the formula  $AA_{-23}-AA_{362}$  of Figure 3, a polypeptide of the formula  $AA_{1-362}$  of Figure 3, a polypeptide of the formula  $Met-AA_{1-362}$  of Figure 3, a polypeptide of the formula  $AA_{1-374}$  of Figure 3, a polypeptide of the formula  $Met-AA_{1-374}$  of Figure 3, a polypeptide of the formula  $AA_{1-377}$  of Figure 3, a polypeptide of the formula  $Met-AA_{1-377}$  of Figure 3, a polypeptide of the formula  $AA_{-23}-AA_{374}$  of Figure 3, a polypeptide of the formula  $AA_{-23}-AA_{377}$  of Figure 3.

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9. The polypeptide according to claim 7, wherein said polypeptide is selected from the group consisting of a polypeptide of the formula AA<sub>-23</sub>-AA<sub>182</sub> of Figure 16, a polypeptide of the formula AA<sub>1</sub>-AA<sub>182</sub> of Figure 16, a polypeptide of the formula Met-AA<sub>1-182</sub> of Figure 16, a polypeptide of the formula AA<sub>-23</sub>-AA<sub>182</sub> of Figure 16, followed by the amino acids asparagine-leucine-glutamine-histidine-serine-leucine, a polypeptide of the formula AA<sub>1</sub>-AA<sub>182</sub> of Figure 16, followed by the amino acids asparagine-leucine-glutamine-histidine-serine-leucine, a polypeptide of the formula Met-AA<sub>1-182</sub> of Figure 16, followed by the amino acids asparagine-leucine-glutamine-histidine-serine-leucine, a polypeptide of the formula AA<sub>-23</sub>-AA<sub>113</sub> of Figure 16, a polypeptide of the formula AA<sub>1</sub>-AA<sub>113</sub> of Figure 16, a polypeptide of the formula Met-AA<sub>1-113</sub> of Figure 16, a polypeptide of the formula AA<sub>-23</sub>-AA<sub>111</sub> of Figure 16, a polypeptide of the formula AA<sub>1</sub>-AA<sub>111</sub> of Figure 16, a polypeptide of the formula Met-AA<sub>1-111</sub> of Figure 16, a polypeptide of the formula AA<sub>-23</sub>-AA<sub>131</sub> of Figure 16, a polypeptide of the formula AA<sub>1</sub>-AA<sub>131</sub> of Figure 16, a polypeptide of the formula Met-AA<sub>1-131</sub> of Figure 16, a polypeptide of the formula AA<sub>-23</sub>-AA<sub>145</sub> of Figure 16, a polypeptide of the formula AA<sub>1</sub>-AA<sub>145</sub> of Figure 16, a polypeptide of the formula Met-AA<sub>1-145</sub> of Figure 16, a polypeptide of the formula AA<sub>-23</sub>-AA<sub>166</sub> of Figure 16, a polypeptide of the formula AA<sub>1</sub>-AA<sub>166</sub> of Figure 16, a polypeptide of the formula Met-AA<sub>1-166</sub> of Figure 16, or portions thereof.

10. The polypeptide according to claim 7, wherein said polypeptide is selected from the group consisting of a polypeptide of the formula AA<sub>-23</sub>-AA<sub>362</sub> of mature T4 protein, a polypeptide of the formula AA<sub>1</sub>-AA<sub>362</sub> of mature T4 protein, a polypeptide of the formula Met-AA<sub>1-362</sub> of mature T4 protein, a polypep-

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tide of the formula  $AA_{1-374}$  of mature T4 protein, a polypeptide of the formula  $Met-AA_{1-374}$  of mature T4 protein, a polypeptide of the formula  $AA_{1-377}$  of mature T4 protein, a polypeptide of the formula  
 5  $Met-AA_{1-377}$  of mature T4 protein, a polypeptide of the formula  $AA_{23-AA_{374}}$  of mature T4 protein, a polypeptide of the formula  $AA_{23-AA_{377}}$  of mature T4 protein, or portions thereof.

11. The polypeptide according to claim 7,  
 10 wherein said polypeptide is selected from the group consisting of a polypeptide of the formula  $AA_{23-AA_{182}}$  of mature T4 protein, a polypeptide of the formula  $AA_1-AA_{182}$  of mature T4 protein, a polypeptide of the formula  $Met-AA_{1-182}$  of mature T4 protein, a polypep-  
 15 tide of the formula  $AA_{23-AA_{182}}$  of mature T4 protein, followed by the amino acids asparagine-leucine-glutamine-histidine-serine-leucine, a polypeptide of the formula  $AA_1-AA_{182}$  of mature T4 protein, followed by the amino acids asparagine-leucine-glutamine-  
 20 histidine-serine-leucine, a polypeptide of the formula  $Met-AA_{1-182}$  of mature T4 protein, followed by the amino acids asparagine-leucine-glutamine-histidine-serine-leucine, a polypeptide of the formula  $AA_{23-AA_{113}}$  of mature T4 protein, a polypeptide of  
 25 the formula  $AA_1-AA_{113}$  of mature T4 protein, a polypeptide of the formula  $Met-AA_{1-113}$  of mature T4 protein, a polypeptide of the formula  $AA_{23-AA_{111}}$  of mature T4 protein, a polypeptide of the formula  $AA_1-AA_{111}$  of mature T4 protein, a polypeptide of the formula  
 30  $Met-AA_{1-111}$  of mature T4 protein, a polypeptide of the formula  $AA_{23-AA_{131}}$  of mature T4 protein, a polypeptide of the formula  $AA_1-AA_{131}$  of mature T4 protein, a polypeptide of the formula  $Met-AA_{1-131}$  of mature T4 protein, a polypeptide of the formula  $AA_{23-AA_{145}}$   
 35 of mature T4 protein, a polypeptide of the formula  $AA_1-AA_{145}$  of mature T4 protein, a polypeptide of the

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formula Met-AA<sub>1-145</sub> of mature T4 protein, a polypeptide of the formula AA<sub>-23-AA<sub>166</sub></sub> of mature T4 protein, a polypeptide of the formula AA<sub>1-AA<sub>166</sub></sub> of mature T4 protein, a polypeptide of the formula Met-AA<sub>1-166</sub> of mature T4 protein, or portions thereof.

12. A method for producing a polypeptide selected from the group consisting of the polypeptides of any one of claims 7 to 11 comprising the step of culturing a unicellular host transformed with a recombinant DNA molecule selected from the group consisting of the recombinant DNA molecules of claim 3 or 4.

13. A pharmaceutical composition comprising an immunotherapeutic or immunosuppressive effective amount of a polypeptide selected from the group consisting of the polypeptides of any one of claims 7 to 11 and a pharmaceutically acceptable carrier.

14. A method for treating patients comprising the step of treating them in a pharmaceutically acceptable manner with a composition selected from the group consisting of the composition of claim 13.

15. The method according to claim 14, wherein the patient is treated by intramuscular injection of the composition.

16. A diagnostic composition for detecting or for monitoring the course of HIV infection comprising a diagnostic effective amount of a polypeptide selected from the group consisting of the polypeptides of any one of claims 7 to 11.

17. A method for detecting or for monitoring the course of HIV infection comprising the

step of employing as a diagnostic a composition selected from the group consisting of the compositions of claim 16.

5 18. A means for detecting or for monitoring the course of HIV infection comprising a composition selected from the group consisting of the compositions of claim 16.

10 19. A pharmaceutical composition comprising an immunotherapeutic or immunosuppressive effective amount of antibody to a polypeptide selected from the group consisting of the polypeptides of any one of claims 7 to 11 and a pharmaceutically acceptable carrier.

15 20. A method for treating patients comprising the step of treating them in a pharmaceutically acceptable manner with a composition according to claim 19.

20 21. The use of a polypeptide selected from the group consisting of the polypeptides of any one of claims 7 to 11 to purify HIV virus.

22. The use according to claim 20, wherein the HIV virus is purified from a biological sample.

25 23. A method for purifying HIV virus from a sample comprising the step of exposing the sample to a polypeptide selected from the group consisting of the polypeptides of any one of claims 7 to 11.

24. The method according to claim 22, wherein the sample is a biological sample.

25. A DNA sequence comprising the DNA insert of p170-2, said sequence coding on expression for a T4-like polypeptide.

5 26. A recombinant DNA molecule comprising a DNA sequence selected from the group consisting of the DNA sequence of claim 25, said DNA sequence being operatively linked to an expression control sequence in said recombinant DNA molecule.

10 27. A unicellular host transformed with a recombinant DNA molecule according to claim 26.

28. A polypeptide coded for on expression by a DNA sequence of claim 25, said polypeptide being essentially free of other proteins of human origin.

15 29. A pharmaceutical composition comprising an immunotherapeutic or immunosuppressive amount of a soluble protein receptor and a pharmaceutically acceptable carrier.

20 30. A method for treating patients comprising the step of treating them in a pharmaceutically acceptable manner with a pharmaceutical composition of claim 29.

25 31. A diagnostic composition for detecting or for monitoring the course of viral infection comprising a diagnostic effective amount of a soluble protein receptor.

32. A method for detecting or for monitoring the course of a viral infection comprising the step of employing as a diagnostic a diagnostic effective amount of a soluble protein receptor.

33. A means for detecting or for monitoring the course of a viral infection comprising a soluble protein receptor.

34. A DNA sequence selected from the group consisting of:

- (a) the DNA insert of pBiv.1;
- (b) DNA sequences which hybridize to the DNA insert of pBiv.1 and which code on expression for a polyvalent soluble T4-like polypeptide; and
- (c) DNA sequences which code on expression for a polyvalent soluble T4-like polypeptide coded for by the DNA insert of pBiv.1.

35. A recombinant DNA molecule comprising a DNA sequence selected from the group consisting of the DNA sequences of claim 34, said DNA sequence being operatively linked to an expression control sequence in said recombinant DNA molecule.

36. A unicellular host transformed with a recombinant DNA molecule according to claim 35.

37. A polypeptide coded for on expression by a DNA sequence selected from the group consisting of the DNA sequences according to claim 34, said polypeptide being essentially free of other proteins of human origin.

38. The polypeptide according to claim 7, wherein said polypeptide is polyvalent.

39. A method for producing a polyvalent polypeptide comprising the steps of:

- (a) culturing a unicellular host transformed with a recombinant DNA molecule according to claim 3 or 4 to produce a polypeptide; and

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(b) coupling said polypeptide to a carrier to form a polyvalent polypeptide.

40. A DNA sequence comprising:

(a) a first portion comprising a DNA sequence coding for the constant region of an immunoglobulin light chain; and

(b) a second portion comprising a DNA sequence according to claim 1 or 2, or portions thereof, said second portion being joined upstream of said first portion.

41. A DNA sequence comprising:

(a) a first portion comprising a DNA sequence coding for the constant region of an immunoglobulin heavy chain; and

(b) a second portion comprising a DNA sequence according to claim 1 or 2, or portions thereof, said second portion being joined upstream of said first portion.

42. An expression vector comprising the DNA sequence according to claim 40.

43. An expression vector comprising the DNA sequence according to claim 41.

44. An expression vector comprising the DNA sequence according to claim 40 and the DNA sequence according to claim 41.

45. A method for producing a chimeric rsT4/IgG<sub>1</sub> comprising the step of co-transfecting a host cell with the expression vector according to claim 42 and the expression vector according to claim 43.

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46. A method for producing a chimeric rsT4/IgG<sub>1</sub> comprising the step of transfecting a host cell with the expression vector according to claim 44.

47. A chimeric rsT4/IgG<sub>1</sub> produced by the method according to claim 45 or 46.

48. A pharmaceutical composition comprising an immunotherapeutic or immunosuppressive effective amount of a polypeptide according to claim 37 or 38.

49. A method for treating patients comprising the step of treating them in a pharmaceutically acceptable manner with a composition according to claim 48.

50. A diagnostic composition for detecting or for monitoring the course of HIV infection comprising a diagnostic effective amount of a polypeptide according to claim 37 or 38.

51. A pharmaceutical composition comprising an immunotherapeutic or immunosuppressive effective amount of a chimeric rsT4/IgG<sub>1</sub> according to claim 47.

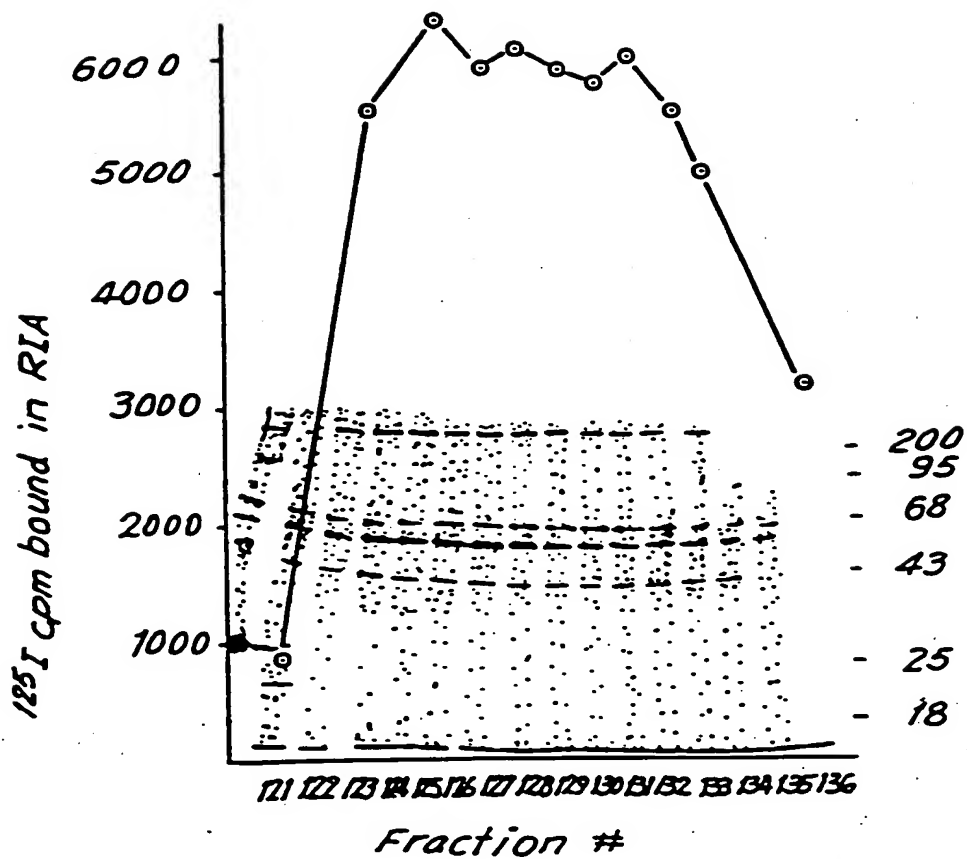
52. A method for treating patients comprising the step of treating them in a pharmaceutically acceptable manner with a composition according to claim 51.

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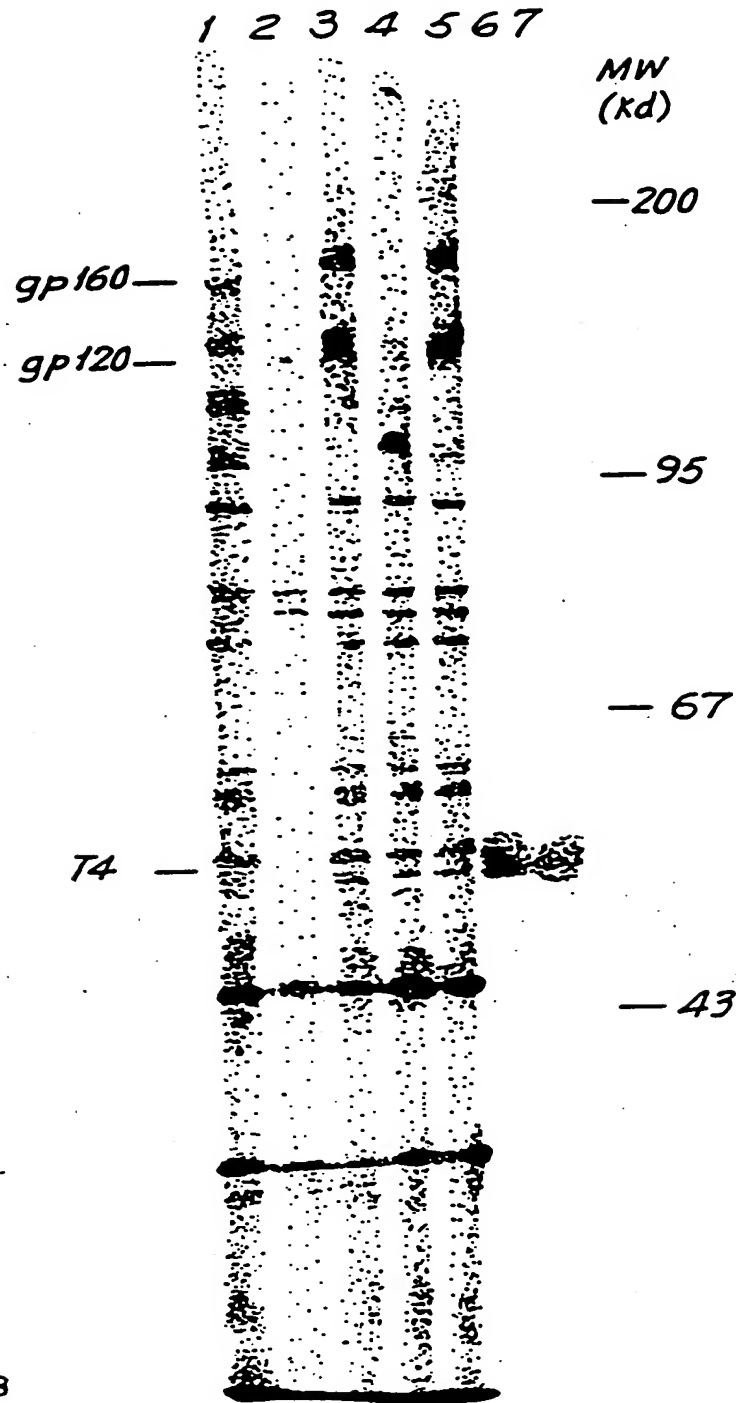
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FIG. 1

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FIG. 2



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**FIG. 3**

H 1 P M M NBsscNC  
 n n s n n laptoR  
 f REX5' t 1 1 an1NRpP  
 1 1 1 1 4221221  
 /////  
 TTTT TTTT TTAAGCAGCACTCTGCAGAAGCAAGCACCCCTCCCACTGGGCTCTCGG 60  
 -----+-----+-----+-----+-----+-----+-----+-----+  
 AAAAAAAAAAATTCGTGCTGAGACGTCTTCCTTGTTTCGTGGGAGGGGTGACCCGAGGACC  
 F F L S T T L Q K E Q S T L P T G L L V -  
 BH  
 A BscN5S M M F N  
 l apisa s n s B BM  
 u nlApct 1 1 up b bn  
 1 221211 1 1 4 B v vl  
 1 1 H 2 1 11  
 /////  
 TTGCAGAGCTCCAAGTCTCACACAGATACGCTGTTTGAGAAGCAGCGGGCAAGAAAGA 120  
 -----+-----+-----+-----+-----+-----+-----+-----+  
 AACGTCTCGAGGTTCAAGGAGTGTGTCTATGCGGACAAACTCTTCGTCCGCCGTTCTTTCT  
 A E L Q V L T Q I R L F E K Q R A R K T -  
 S B B P S S  
 M H HDHaP s DBsNADNpPaS D DHNPa  
 n g graus t dapevrlusui d ralsu  
 1 a aa09s X enlpasaaMs9n e aaas9  
 1 1 12361 1 12222241161 1 23416  
 // / // / /  
 CGCAAGCCCAGAGCCCTGCCATTCTGTGGGCTCAGGTCCCTACTGGCTCAGGCCCCCTG 180  
 -----+-----+-----+-----+-----+-----+-----+-----+  
 GCGTTCGGGTCTCCGGACGGTAAGACACCCGAGTCCAGGGATGACCGAGTCCGGGGAC  
 Q A Q R P C H F C G L R S L L A Q A P A -  
 REX Splice  
 Donor S H F  
 M M MEM HMNC i B B n  
 n n nan pscr n b b u  
 1 1 lel apif f v v 4  
 1 1 131 Met 2111 1 i 1 H  
 ///  
 CCTCCCTCGCAAGGCCACATGACCGGGGAGTCCCTTTTAGGCACTTGCTTCTGGTGC 240  
 -----+-----+-----+-----+-----+-----+-----+-----+  
 GGAGGGAGCCGTTCCGGTGTACTTGCCCCCTCAGGGAAAATCGTGAACGAAGACCACG  
 S L G K A T M N R G V P F R H L L L V L -  
 AA-23  
 H F  
 i HH nM M D B B  
 n ha un n d b b  
 P ae 4l l e v v  
 1 12 H1 1 1 1 1  
 TGCAACTGGCGCTCCTCCAGCAGCCACTCAGGGAAAGAAAGTGGTGCTGGGCAAAAAAG 300  
 -----+-----+-----+-----+-----+-----+-----+-----+  
 ACGTTGACCGCGAGGAGGGTCTGTCGGTGAGTCCCTTTCTTTTACCACGACCCGTTTTTTC  
 Q L A L L P A A T Q G K K V V L G K K G -  
 R A AA1  
 s l  
 a u  
 1 1  
 H M M M  
 b bb b  
 o oo o  
 2 22 2  
 GGGATACAGTGGAACTGACCTGTACAGCTTCCAGAGAAGAGCATACAATTCCACTGGA 360  
 -----+-----+-----+-----+-----+-----+-----+-----+  
 CCCTATGTCTACCTTGACTGGACATGTGGAAGGGTCTTCTTCTCGTATGTTAAGGTGACCT  
 D T V E L T C G T A A S F P K K S I Q F H W K -

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## FIG 3(cont'd)

	H		B		S
	i		NBS*	F	AAS
	n		laps	o	vui
	f		anlp	k	a9n
	1		4222	1	261
			//		//

361 AAAACTCCAACCAGATAAAGATTCTCGGAAATCAGGGCTCCTTCTTAAGTAAAGGTCCAT 420  
 TTTTGAGGTTGGTCTATTTCCTAAGACCCTTTAGTCCCGAGGAAGAATTGATTTCAGGTA  
 N S N Q I K I L G N Q G S F L T K G P S -

	S	PH	H		S	REX
A	MNDa	niHT	i	M	MANaSS	Splice
1	bdpu	unhh	n	b	bvluit	Acceptor
u	oen3	DPaa	f	o	oaz9ny	
1	121A	2111	1	2	224611	
		//			//	

421 CCAAGCTGAATGATCGCGCTGACTCAAGAAGAAGCCTTCGGGACCAAGGAACTTTCCCC 480  
 GGTTCGACTTACTAGCGCGACTGAGTTCTTCTTCGGAAGCCCTGGTTCCTTTGAAAGGGG  
 K L N D R A D S R R S L R D Q G N F P L -

	S	H		H		S
BMDNa	i	A		i D M M		MANMaM
cbpdu	n	f		n d b b		nvnvnn
lone3	f	1		f e o o		lall91
1112A	1	2		1 1 2 2		121161
		//				/

481 TGATCATCAAGAATCTTAAGATAGAAGACTCAGATACTTACATCTGTGAAGTGGAGGACC 540  
 ACTAGTAGTCTTAGAATTCTATCTTCTGAGTCTATGAATGTAGACACTTCACCTCCTGG  
 I I K N L K I E D S D T Y I C E V E D Q -

S		M		E
i		a		c
n		e		o
1		1		B
/				

541 AGAAGGAGGAGGTGCAATTCCTAGTGTTCGGATTGACTGCCAACTCTGACACCCACCTGC 600  
 TCTTCCTCCTCCACGTPAAGCATCACAAGCCTAACTGACGGTTGAGACTGTGGGTGGACG  
 K E E V Q L L V F G L T A N S D T H L L -

B	B		BBE S	
s	s		BascNC	D
P	P	S	aptosr	d
M	M	t	n1NRpF	e
1	1	y	221221	1
		1		
			//	

601 TTCAGGGGCAGAGCCTGACCCTGACCTTGGAGAGCCCCCTGGTAGTAGCCCCCTCAGTGC 660  
 AAGTCCCCGTCTCGGACTGGGACTGGAACCTCTCGGGGGGACCATCATCGGGGAGTCACG  
 Q G Q S L T L T L E S P P G S S P S V Q -

M	M	H		M	M	M	DM	As
n	n	i		b	b	n	dn	lp
1	1	n		o	o	1	el	uB
1	1	f		2	2	1	11	12
		1						/
								/

661 AATGTAGGAGTCCAAGGGGTAAAAACATACAGGGGGGAAGACCCTCTCCGTGTCTCAGC 720  
 TTACATCCTCAGGTTCCCCATTTTGTATGTCCCCCCTTCTGGGAGAGGCACAGAGTCG  
 C R S P R G K N I Q G G K T L S V S Q L -

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*FIG. 3(cont'd)*

M	NH	A	HS	M	MM	M
b	ba	l	at	n	nn	n
o	eo	u	eu	l	ll	l
2	ll	l	3l	l	ll	l

א  
י  
ח  
י

			P	S
A	M M	H	M H M M M O N D A	
l	n n	P	n p a n l a b c p u	
u	l l	b	l h l l M l o e n z	
l	l l	l	l l l l l l l l z l A	

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				B	BES	P	S
M	M	M	M	sM	scc	ADNpPDa	A
n	n	b	b	ta	tor	vr lusdui	l
1	1	o	o	Ee	NRF	aaaMse9n	u
1	1	2	2	23	121	22411161	1

A	H	H	BE S	M	SCMC	HS	D	M	M	H
1	p	p	n	conr	at	d	n	n	p	
u	b	b	1	NR1P	eu	e	1	1	b	
1	1	1	1	1211	31	1	1	1	1	

1021: TGGGCAAGAAGCTCCCGCTCCACCTCACCCTGCCCCAGGCCTTGCCTCAGTATGCTGGCT 1080  
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  
ACCCGTTCTTCGAGGGCGAGGTGGAGTGGGACGGGGTCCGGAACGGAGTCATACGACCGA  
G K K L P L H L T L P Q A L P Q Y A G S -

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## FIG. 3(cont'd)

H	BES	S				S	S	BES
P	SCC	MHMa				f	f	SCC
h	tor	nanu				a	a	tor
1	NRF	le19				N	N	NRF
	121	1316				1	1	121

CTGGAAACCTCACCCCTGGCCCTTGAAGCGAAAACAGGAAAGTTGCATCAGGAAGTGAACC 1140  
 -----  
 GACCTTTGGAGTGGGACCGGGAACCTTCGCTTTTGTCTTTCAACGTAGTCCTTCACTTGG  
 G N L T L A L E A K T G K L H Q E V N L -

						P	S
H	H D	A		M M		ADNNpPa	
P	P d	1		n n		villusu	
h	h e	u		1 1		aaaaMs9	
1	1 1	1		1 1		2244116	

TGGTGGTGTATGAGAGCCACTCAGCTCCAGAAAATTGACCTGTGAGGTGTGGGGACCCA 1200  
 -----  
 ACCACCACTACTCTCGGTGAGTGGAGGTCTTTTAACTGGACACTCCACACCCCTGGGT  
 V V M R A T Q L Q K N L T C E V W G P T -

S	S					T
f	Df	MAM	DE	A	M M	a
i	a	da nln	ds	1	n n	q
n	N	eN lul	ep	u	1 1	1
1	1	11 111	11	1	1 1	

CCTCCCCTAAGCTGATGCTGAGCTTGAAACTGGAGAACAGGAGGCAAGGTCTCGAAGC 1260  
 -----  
 GGAGGGGATTGACTACGACTCGAACTTTGACCTCTTGTTCCTCCGTTTCCAGAGCTTCG  
 S P K L M L S L K L E N K E A K V S K R -

			M M	DM		F	FD	M	H
			n n	ds		o	od	a	i
			1 1	et		k	ke	e	n
			1 1	12		1	11	3	1

GGGAGAAGGCGGTGTGGGTGCTGAACCTGAGCGGGGATGTGGCAGTGTCTGCTGAGTG 1320  
 -----  
 CCCTCTTTCGGCCACACCCACGACTTGGGACTCCGCCCTACACCGTCACAGACGACTCAC  
 E K A V W V L N P E A G M W Q C L L S D -

		P	S		H		S		S
A		AdpPaS		i		ANaS		HDNC	
v		vrusui		n		vlui		pscr	
a		aaMs9n		f		aa9n		apiP	
1		221161		1		2361		2111	

ACTCGGGACAGGTCTCTGCTGGAATCCAACATCAAGGTTCTGCCACATGGTCCACCCCGG 1380  
 -----  
 TGAGCCCTGTCCAGGACGACCTTAGGTTGTAGTTCCAAGACGGGTGTACCAGGTGGGGCC  
 S G Q V L L E S N I K V L P T W S T P V -

F		S				H			
n		aH B	B	H	H	Ag	HDNH	M M	M
u		ua b	b	g	g	hi	psaa	n n	b
4		9e v	v	a	a	aD	spee	1 1	o
H		63 1	1	1	1	21	2113	1 1	2

TGCAGCCAATGGCCCTGATTGTGCTGGGGCGTGGCCGGCCCTCTGCTTTTCATTGGGC 1440  
 -----  
 ACGTCGGTTACCGGGACTAACACGACCCCCCGCAGCGCGCGGAGGACGAAAAGTAACCCG  
 Q P M A L I V L G G V A G L L L F I G L -

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## FIG. 3(cont'd)

M S S B N HMBNN H H BAQHBMHNN D  
 b f f a l psaal shihbanal d  
 o N N n a apnea naDaePra e  
 2 1 1 1 4 21114 121112114 1

TAGGCATCTTCTTCTGTGTCTCAGGTGCCGGCACCGAAGCGCCAGCAGAGCGGATGTCTC  
 1441 ----- 1500  
 ATCCGTAGAAGAAGACACAGTCCACGGCCGTGGCTTCCGCGGTTCGTCTCGCCTACAGAG

G I F F C V R C R H R R R Q A E R M S Q -

S H B BB  
 MNDaP F l D M M MH MH Ms ssn HM M M  
 bdpuo o n d n n bp bbb bp pps ps n n  
 oen3k k f e 1 1 oh ooh oM lmp ap 1 1  
 121A1 1 1 1 1 1 21 221 21 212 21 1 1

AGATCAAGAGACTCCTCAGTGAAGAAGACCTGCCAGTGCCTTCACCGGTTTCAGAAGA  
 1501 ----- 1560  
 TCTAGTCTCTGAGGAGTCACTCTTCTTCTGACGGTCACGGGAGTGGCCAAAGTCTTCT

I K R L L S E K K T C Q C P H R P Q K T -

N BE S S F BES  
 MNDMs M M schc MNDaX n ecc BM BM  
 bnlnbp n n toar bdpub u tor bn bn  
 olaloH 1 1 NRfP oen3o 4 NRP vl vl  
 213121 1 1 1231 121A2 H 121 11 11

Stop REX Stop  
 CATGTAGCCCCATTTGAGCGCAGGCGCCAGGCAGATCCCATTGAGCCTCCCCAGGTGT  
 1561 ----- 1620  
 GTACATCGGGGTAAACTCCGTGCTCCGGTCCGTCTAGCGGTGAACGTCGGAGCGGTCCACA

C S P I G T R P G R S H L Q P P Q V S -

F S SBES B  
 nt AaS MNDasccX HS s H M  
 uh vui bdputorh at t z n  
 Da a9n oen3NRfo eu X e l  
 21 261 121A1212 31 1 3 1

CTGCCCCCGGTTTCTGCTGCGGACCAGATGAATGTAGCAGATCCCAGGCTCTGGCCT  
 1621 ----- 1680  
 GACGGGGGCCAAAGGACGGACGCTGGTCTACTTACATCGTCTAGGGTCCGGAGACCGGA

A P R P L P A D Q M N V A D P R P L A S -

M M M BES SS  
 n M M scc DHNPHDNac  
 1 n n tor ralspcur  
 1 1 1 NRP aeasapi9F  
 1 1 1 121 234121161

CCTGPTCGCCTCCTCTACAATTTGCCATTGTTCTCCTGGGTTAGGCCCCGGCTTCACTG  
 1681 ----- 1740  
 GGACAAGCGGAGGAGATGTTAAACGGTAACAAGAGGACCCAATCCGGGGCCGAAGTGAC

C S P P L Q P A I V S P G L G P G F T G -

3763 MMH MM  
 nnn n n  
 lol 1 1  
 111 1 1

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GTTGAGTGTGCTCTCTAGTTTCCAGAGCCTTAATCACACCGTCTTCCAGGCCATTTCCT  
 1741 ----- 1800  
 CAACTCACAACGAGAGATCAAAGGTCTCCGAATTAGTGTGGCAGGAGGTGCGGTAAAGGA

V L L S S P Q R L N H T V L H A I S F -

FIG. 3(cont'd)

S P K P S P S L I I S L • P S P H C S P -

G S Q C S V Q C Q P W L A G C • G W V S -

G S M E H G T V L L Q D R T L G P Q R A -

G T C T K S H S Q A S Q G W H Q I Q R F -

L A A S T S C P M L P A S H P M W V G P -

M	M	NR
D	D	18
1	1	22
1	1	31

Q T H I L T L H K Q P L W T Q P H V H G -



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## FIG. 3(cont'd)

H F F M M F F M M D  
 a o o n n o o n n d  
 e k k l l k k l l e  
 3 1 1 1 1 1 1 1 1 1  
 2161 GCCTCAAGGGATGTCTCACATCCTCTGTCTATTTGAGACTTAGAAAAATCCTACAAGGCT 2220  
 -----  
 CGGAGTTCCCTACAGAGTGTAGGAGACAGATAAACTCTGAATCTTTTATAGGATGTTCCGA  
 L K G C L T S S V Y L R L R K I L Q G W -  
 S  
 A D BMDNa BH  
 C d cbpdu M M ADBaCHSS  
 C e lone3 n n ldapias  
 I 1 1112A 1 1 uenlapct  
 1 1 112111 1 1 11211211  
 // // /////  
 2221 GGCAGTAGACAGAACTAAGATGATCATCTCCAGTTTATAGACCAGAACCAGAGCTCAGAG 2280  
 -----  
 CCGTCATCTGTCTTGATTCTACTAGTAGAGGTCAAATATCTGGTCTTGGTCTCGAGTCTC  
 Q • T E L R • S S P V Y R P E P E L R E -  
 H M H H BES  
 a ps a 1 SCC  
 e ap e n tor  
 1 21 1 1 NRP  
 121  
 /  
 2281 AGGCTAGATGATTGATTACCAAGTGCCGGACTAGCAAGTGCTGGAGTCGGGACTAACCCA 2340  
 -----  
 TCCGATCTACTAATAATGGTTACGGCCTGATCGTTCACGACCTCAGCCCTGATTGGGT  
 A R • L I T K C R T S K C W S R D • P R -  
 P S F B M MB H H  
 ADNpPaS n u s n ns P P  
 vrlusui b b 4 m 1 lm h h  
 aaMs9n v v H 1 1 1 1  
 2241161 1 1  
 // // /////  
 2341 GGTCCCTTGTCCTCAAGTTCCTACTGCTGCTCTTGAATGCAGGGACAAATGCCACACGGCT 2400  
 -----  
 CCAGGGAACAGGGTTCAAGGTGACGACGGAGAACTTACGTCCCTGTTTACGGGTGTGCCGA  
 S L V P S S T A A S • M Q G Q M P H G S -  
 H R R  
 a s s  
 e a a  
 1 1 1  
 2401 CTCACCAGTGGCTAGTGGTGGGTACTCAATGTGTACTTTTGGGTTACAGAAGCACAGCA 2460  
 -----  
 GAGTGGTCACCGATCACCACCCATGAGTTACACATGAAAACCCAAGTGTCTTCGTGTCTGT  
 H Q W L V V G T Q C V L L G S Q K H S T -  
 S  
 SN N ANaS D HS F P MFH  
 tc 1 vlui d at o o non  
 yo a aa9n e eu k k lkl  
 11 3 2461 1 31 1 1 111  
 // // /////  
 2461 CCCATGGGAAGGGTCCATCTCAGAGAATTTACGAGCAGGGATGAAGGCCTCCCTGTCTAA 2520  
 -----  
 GGGTACCCCTCCAGGTAGAGTCTCTTAAATGCTCGTCCCTACTTCCGGAGGGACAGATT  
 3765 H G K G P S Q R I Y E Q G • R P P C L K -

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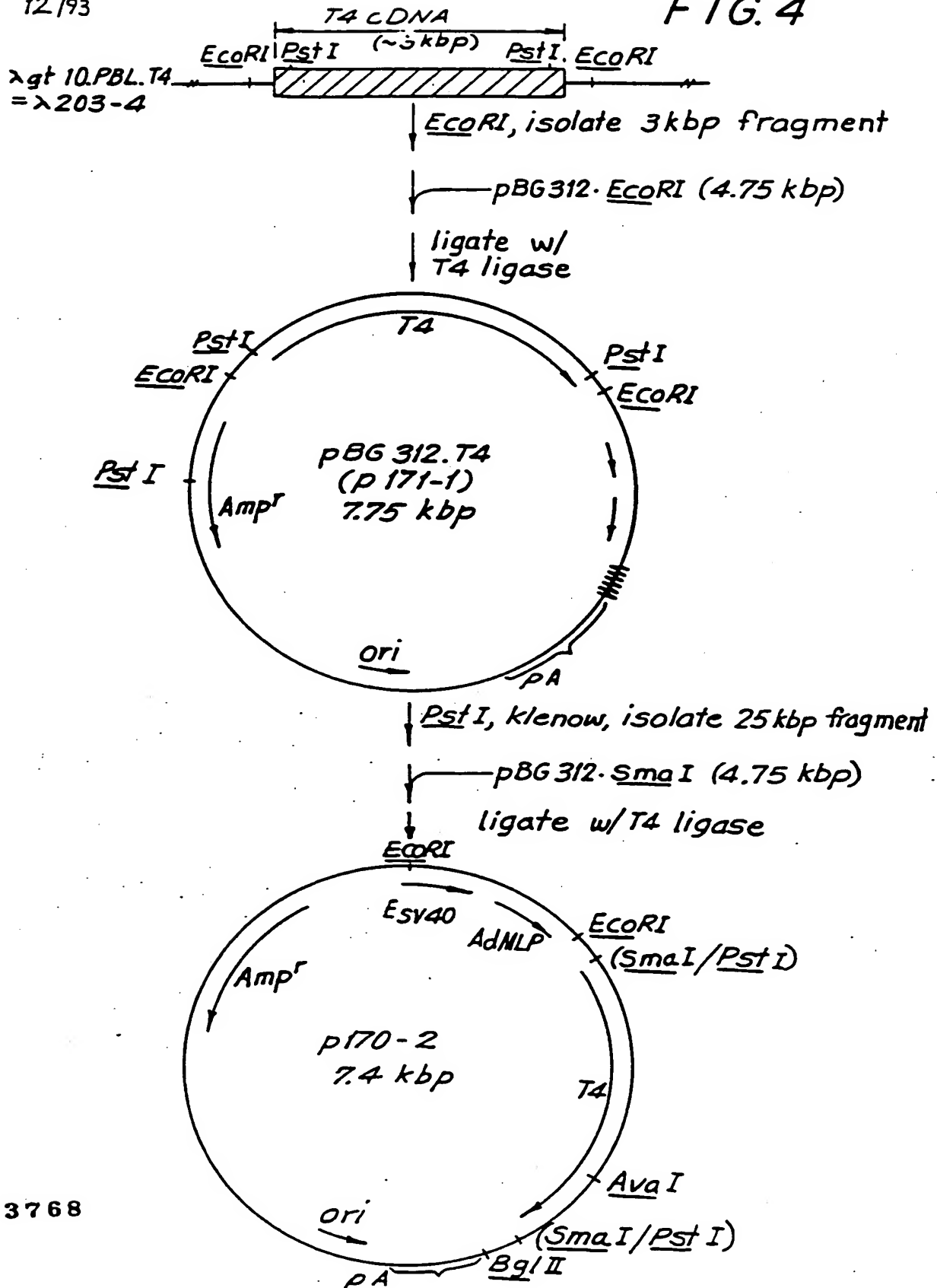
# FIG. 3(cont'd)

	F		M M	N		H		i M MM		M	M	
	o		n n	p		n n na		b b		b	b	
	k		l l	B		f l le		o o		o	o	
	l		l l	2		l l 13		2 2		2	2	
2521	AATCCCTCCTTCATCCCCCGCTGGTGGCAGAATCTGTTACCAGAGGACAAAGCCTTTGGC											2580
	TTAGGGAGGAAGTAGGGGGCGACCACCGTCTTAGACAATGGTCTCCTGTTTCGGAAACCG											
	S L L H P P L V A E S V T R G Q S L W L -											
			H			BH						
			i H	A		sqN	P	B	B M			
			n h	l		pis	s	s	s a			
			P a	u		lap	t	m	m e			
			l l	1		212	1	1	1 3			
	//											
2581	TCTTCTAATCAGAGCGCAAGCTGGGAGCACAGGCACTGCAGGAGAGAATGCCCCAGTGACC											2640
	AGAAGATTAGTCTCGCGTTTCGACCCTCGTGTCGGTGACGTCCTCTCTTACGGGCTCACTGG											
	F * S E R K L G A Q A L Q E R M P S D Q -											
					BES							
	M		scc	M M	AM M				MAAMN			
	a		cor	n n	ln n				nlanh			
	e		NRP	l l	ul l				luele			
	3		121	l l	11 1				11111			
	//											
2641	AGTCACTGACCCCTGTGCAGAACCTCCTCGAAGCGAGCTTTGCTGGGAGAGGGGGTAGCTA											2700
	TCAGTGACTGGGACACGTCTTGGAGGACCTTCGCTCGAAACGACCCTCTCCCCATCGAT											
	S L T L C R T S W K R A L L G E G V A S -											
					P S			BES		H		
	D	N	D	ADMMNPas	M M	HaccH		i H				
	d	1	d	vrnnlusui	n n	ptorp		n h				
	e	a	e	aallaMs9n	l l	hNRFh		P a				
	1	4	1	221141161	1 1	11211		1 1				
	//											
2701	GCCTGAGAGGGGAACCCCTCTAAGGGACCTCAAAGGTGATTGTGCCAGGCTCTGCGCCTGCC											2760
	CGGACTCTCCCTTGGGAGATTCCCTGGAGTTTCCACTAACACGGTCCGAGACGCGGACGG											
	L R G N P L R D L K G D C A R L C A C P -											
			M M		M M M			M	MM			
			n n		n nn n			b	ab			
			l l		l 11 1			o	eo			
			1 1		1 11 1			2	32			
2761	CCACACCCCTCCCTTACCCTCCTCCAGACCATTCAGGACACAGGGAAATCAGGGTTACAAA											2820
	GGTGTGGGAGGGGAATGGGAGGAGGTCTGGTAAGTCTGTGTCCCTTTAGTCCCAATGTTT											
	T P S L T L L Q T I Q D T G K S G L Q I -											
			S		B	S						
	MNDa		D M	ADMMNNAI	H M	HM		M M D				
	bdpu		d b	mbpbdluh	p n	pn		n n d				
	oen3		e o	Honoa3o	h l	hl		l l e				
	121A		1 2	111224A2	1 1	11		1 1 1				
	//											
2821	TCTTCTTGATCCACTTCTCTCAGGATCCCTCTCTTCCCTACCCTTCCTCACCCTTCCCT											2880
	AGAAGAAGTGGTGAAGAGAGTCTAGGGGAGAGAAGGATGGGAAGGAGTGGTGAAGGGA											
	F L I H P S Q D P L S S Y P S S P L P S -											



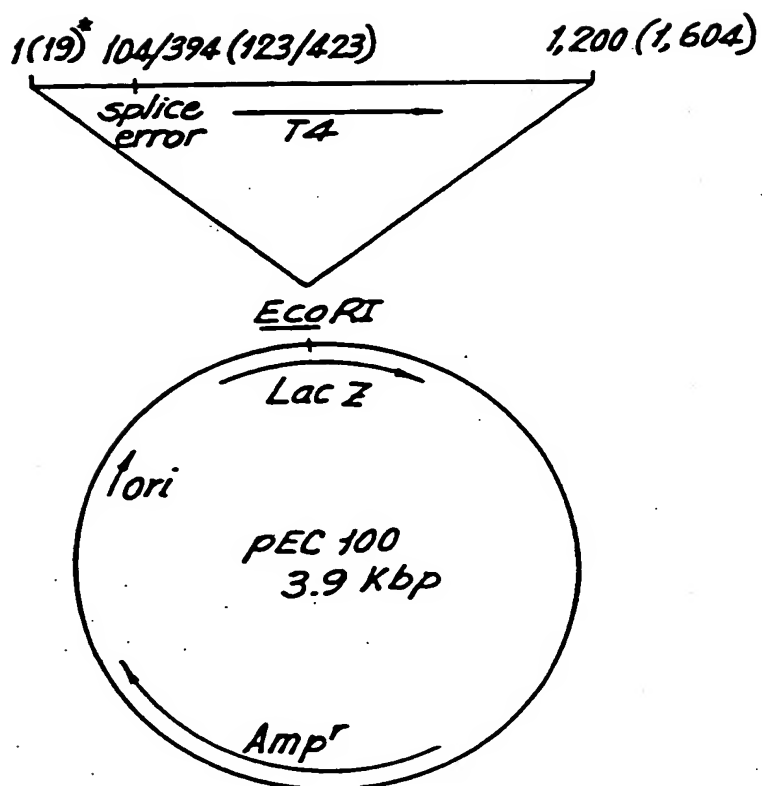
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FIG. 4



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FIG. 5



\* numbers in parentheses refer to PBL T4 cDNA coordinates

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## FIG. 6

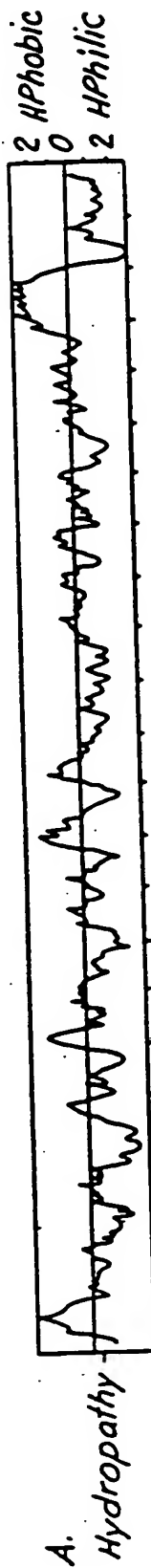
AMINO ACID SEQUENCE COMPARISON AT POSITIONS 36 AND 231 OF T4

Position No.	Maddon et al.	PBL Clone	Rex Clone	Genomic	Mouse	Sheep
3	N AAC	K AAG	-	-	K AAG	K -
64	W TGG	R CGG	W TGG	W TGG	W TGG	-
231	F TTT	S TCT	F TTT	-	F TTC	-

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KYLPTWSTPVQPMALIVLGGVAGLLIFIGLIGFCVRCRHR

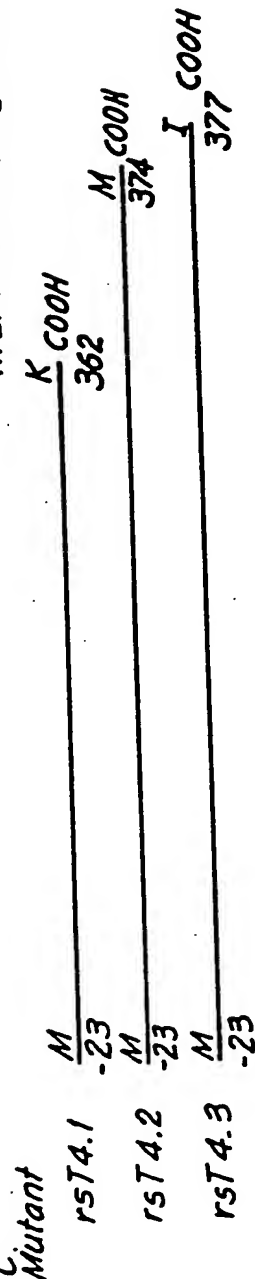


FIG. 7A

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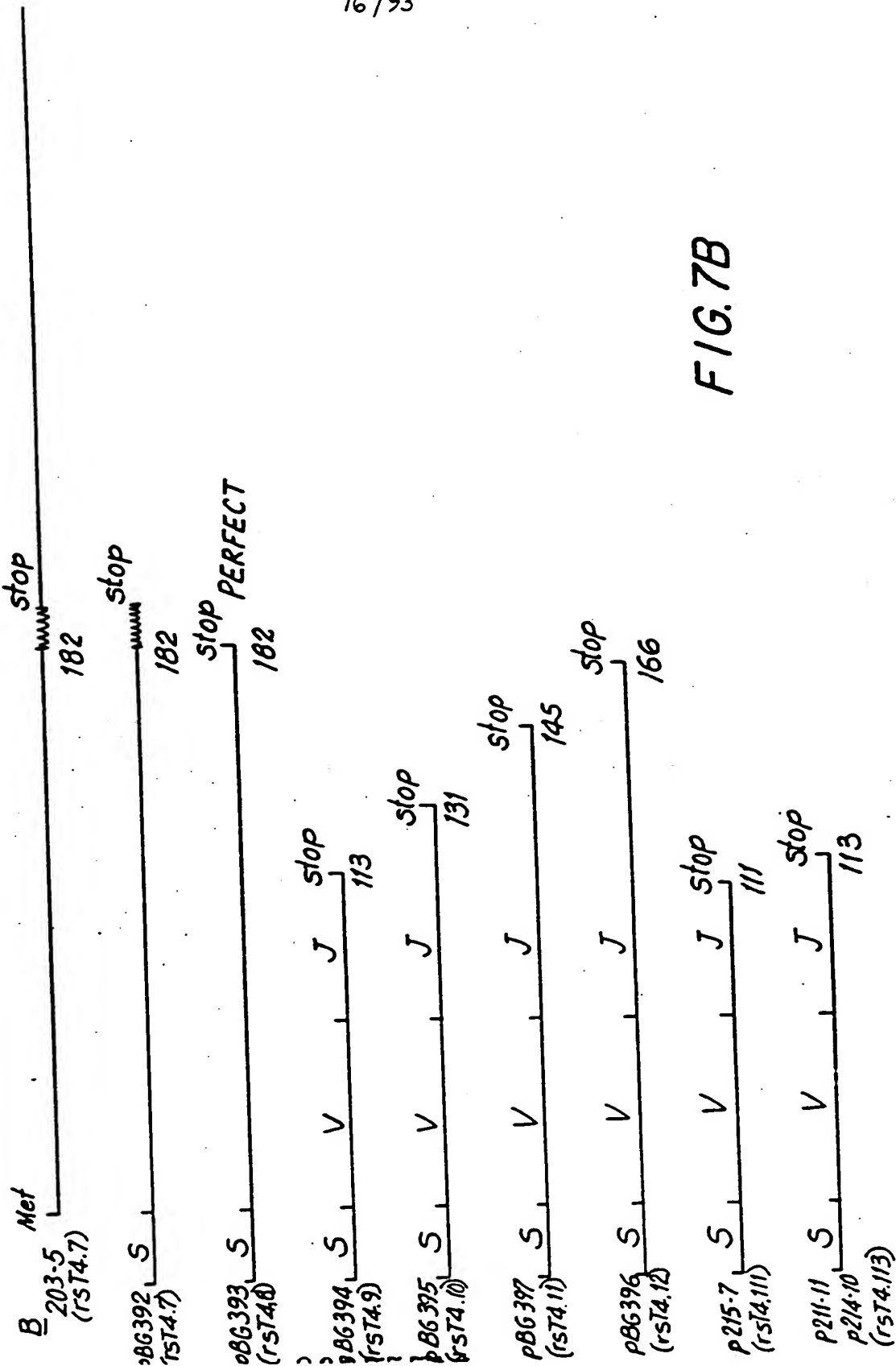
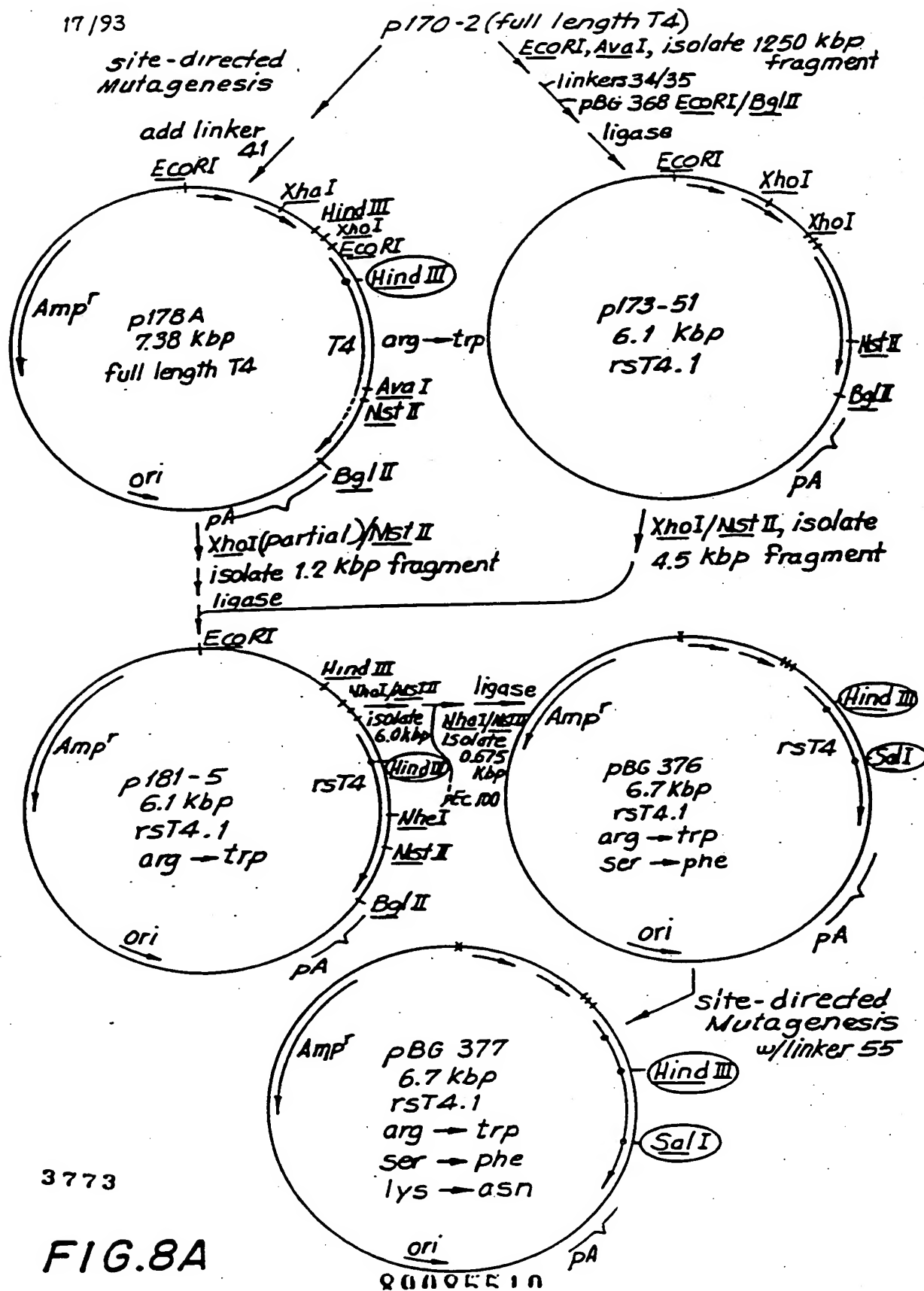


FIG. 7B

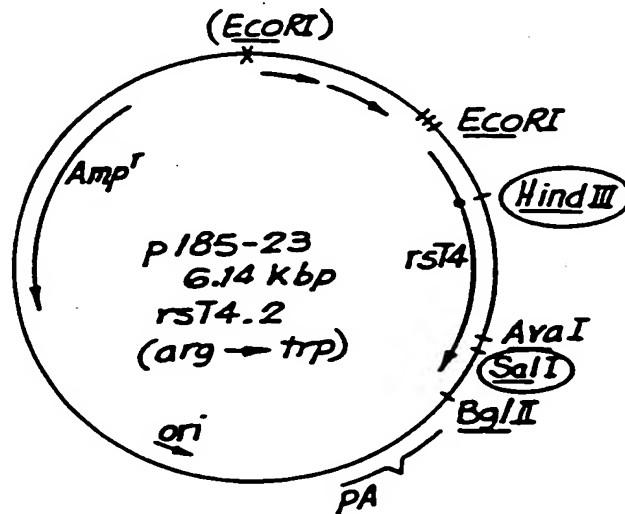




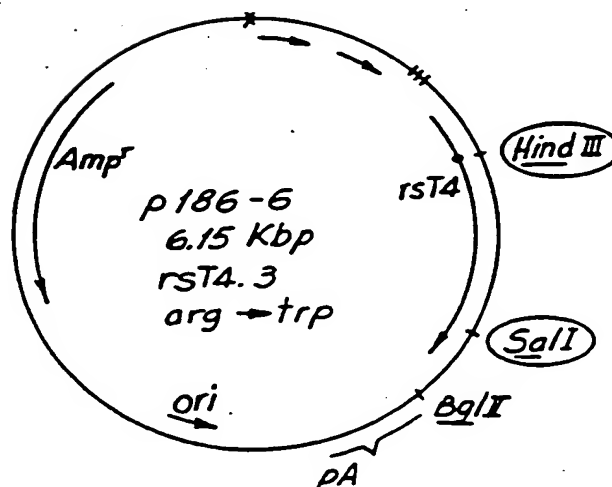
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**FIG. 8B** p178A (full length T4)arg → trp ↓ Ava I, Eco RI, Isolate 1.2 kbp fragmentLinkers 46/47, 48/49  
pBG 368-Eco RI/Bgl II

↓ Ligase

↓ Eco RI/Sal I, Isolate 1.3 kbp fragment

Linkers 50/51

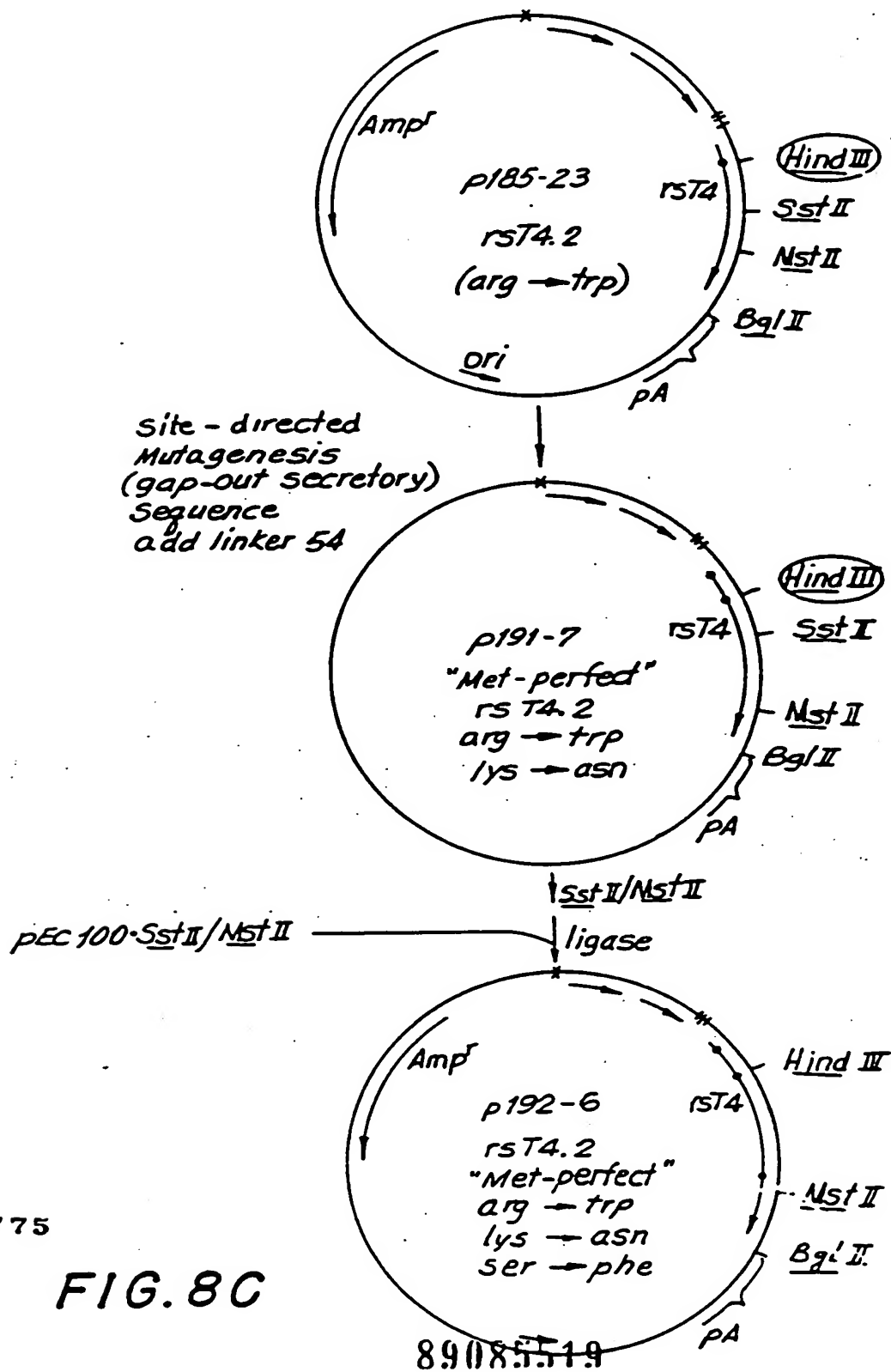
pBG 368-Eco RI/Bgl II

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"Met-perfect" cassette for *E. coli* expression of *rsT4*



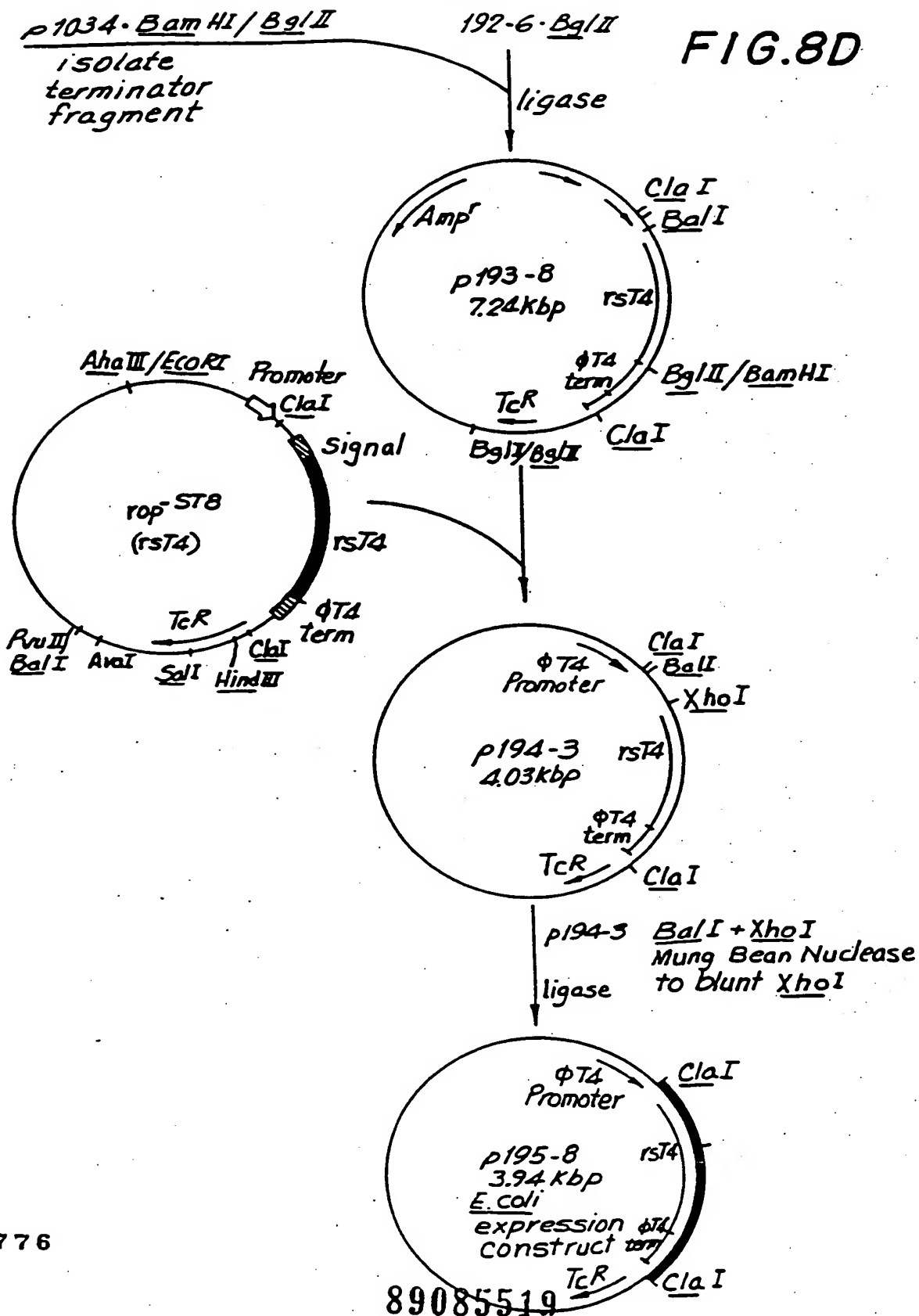
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FIG. 8C

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FIG.8D

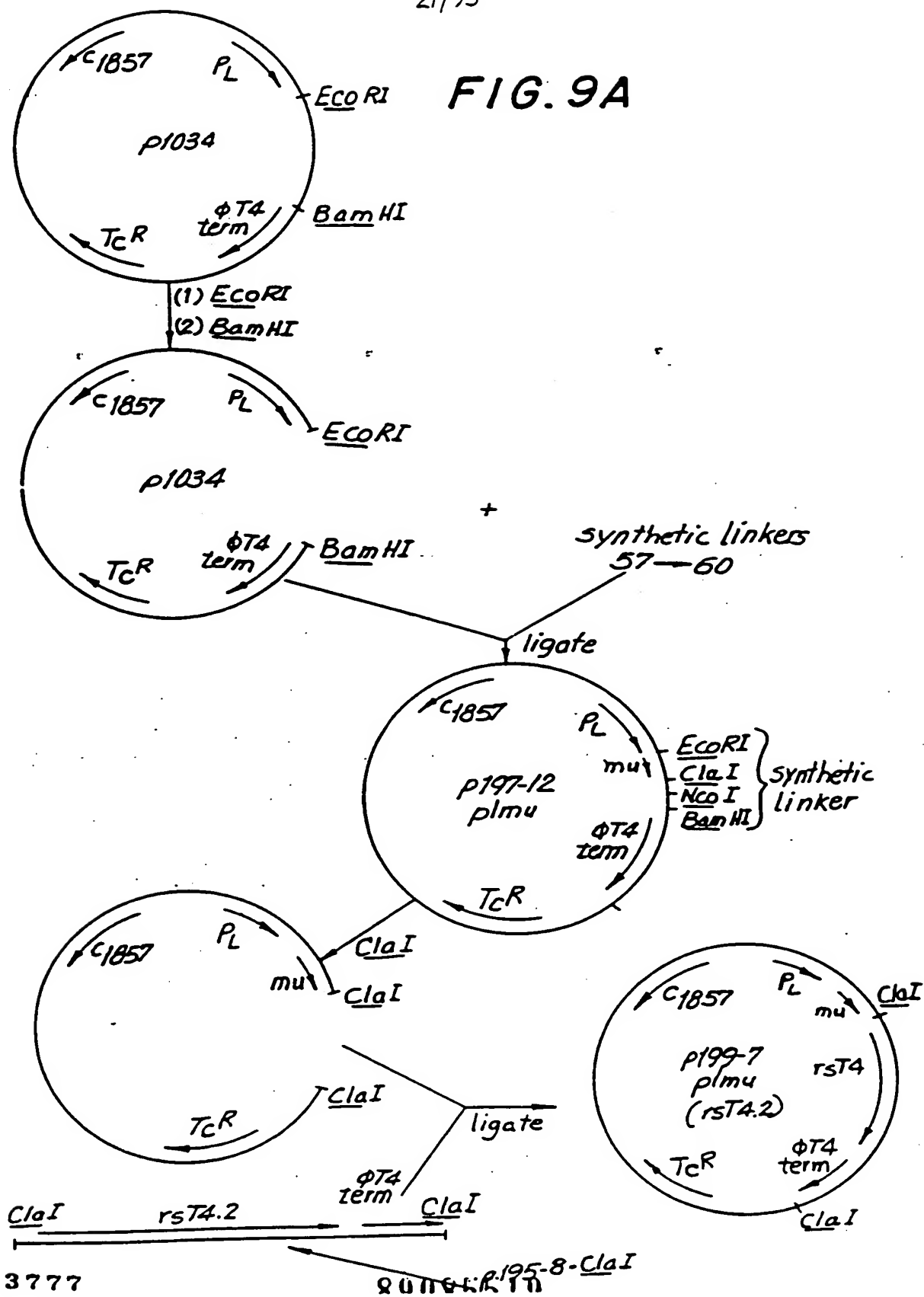


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FIG. 9A



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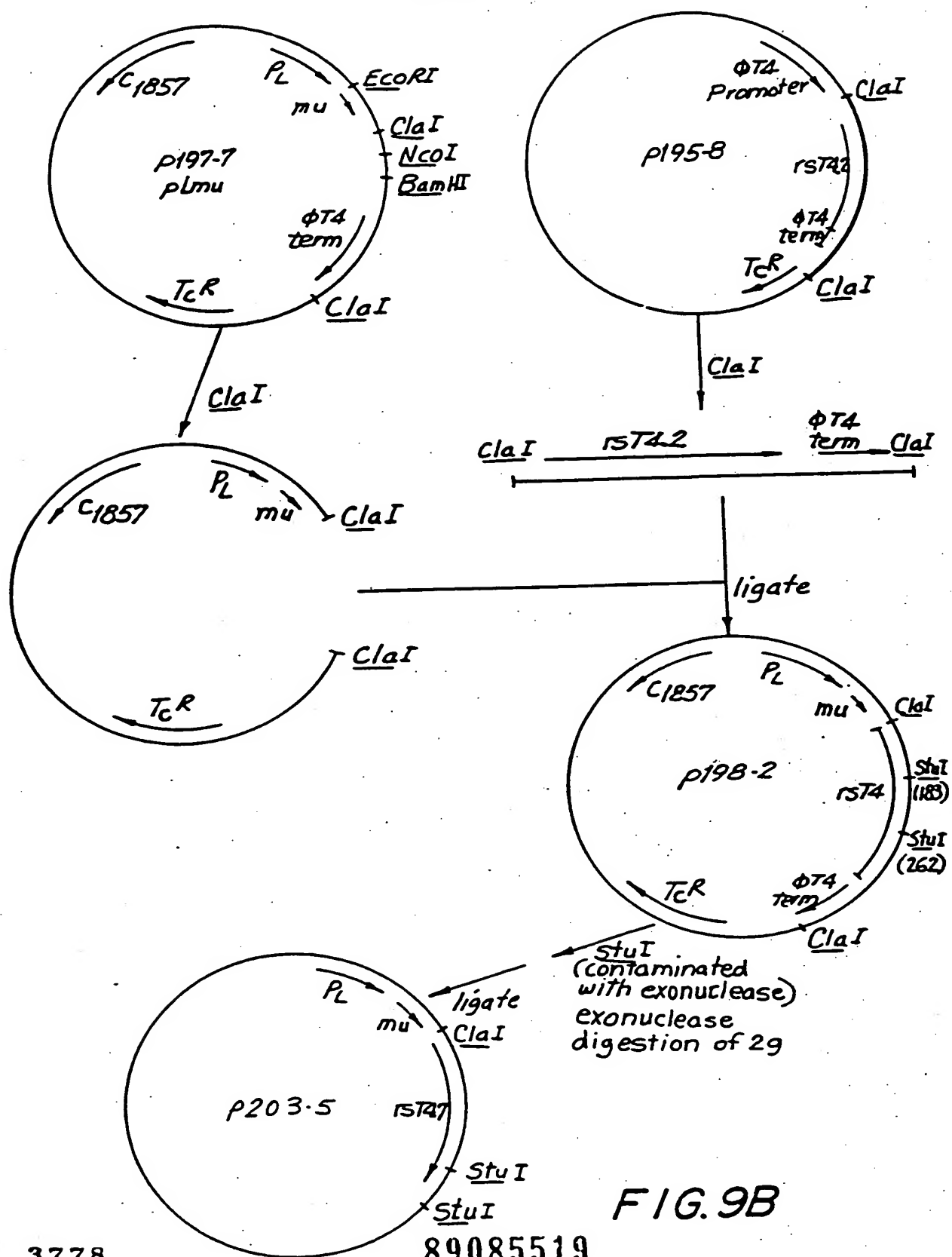


FIG. 9B

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# FIG. 9C

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	180					<u>StuI</u>				
CTA	GCT	TTC	CAG	AAG	<u>GCC</u>	TCC	AGC	ATA	GTC	TAI
					deletion					

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	180		182							
CTA	GCT	TTC	CAG	AAC	CTC	CAG	CAT	AGT	CTA	TAA
leu	ala	phe	gln	asn	leu	gln	his	ser	leu	stop
				←T4 frameshift→						

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*FIG. 10*48

5' CTG CCC ACA TCG TCG ACC CCG GTG CAG CCA ATG TGA 3'

49

5' GAT CTC ACA TTG GGT GCA CCG GGG TCG ACC ATG T 3'

50

5' TCG ACC CCG GTG CAG CCA ATG GCC CTG ATT TGA 3'

3' GG GGC CAC GTC GGT TAC CCG GAC TAA ACT CTA G 5'

5141

5' GAA GAA GGT TGT GGG ACC AAG 3'

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5' TCG GGA CAG GTC CTG CTG GAA TCC AAC ATC AAG TGA A 3'

3' CTG TCC AGG ACC ACC TTA GGT TGT AGT TCA CTT CTA G 5'

3555

5' CAG CCA CCC AAG GAA ACA AAG TCG 3'

46

5' TCG GGA CAG GTC CTG CTG GAA TCC AAC ATC AAG GTT 3'

47

5' GCG CAG AAC CTT GAT GTT GGA TTC CAG CAG CAC CTG TC 3'

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*FIG. 10(cont'd)*54

5' AGC TTC GAC TCG ACC ATG CAG CGA AAC AAA GTG GTG 3'

← 57 58  
5' AATTCCTTACACTTAAATTGCTAACTTTATAGATTACAAACTT  
GAATGTGAATCAATTAAACGATTGAAATATCTAATGTTTGA  
59 →

ACGAAATCGATTTCATCG

TCCTTTAGCTAAAGGTACCTAG 5'  
60 →

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## FIG. 11(cont'd)

361 GTGTTGGGATTGACTGCCAACTCTGACACCCACCTGCTTCAGGGCCAGACCTGACCTG 420  
 CACAAGCCTAACTGACGGTTGAGACTGTGGGTGGACGAAGTCCCCGTCTCCGACTGGGAC  
 ValPheGlyLeuThrAlaAsnSerAspThrHisLeuLeuGlnGlyGlnSerLeuThrLeu -

S BBE S H S  
 c BaccNC d M i c  
 y aptoor e l 1 y  
 1 nlnrpf 1 1 1  
 1 221221 / ///  
 421 ACCTTCGAGAGCCCCCTGGTAGTAGCCCTCAGTGCATGTAGGAGTCCAAGCGGTAA 480  
 TCGAACCTCTCGGGGGGACCATCATCGGGGAGTCACGTTACATCTCAGGTTCCCCATT  
 ThrLeuGluSerProProGlySerSerProSerValGlnCysArgSerProArgGlyLys -

M M D N BBEH SB BES  
 b n d AsP A BaccGNSCS B Nacc  
 o l e lpv l aptoisarts a ltor  
 2 1 1 uBu u nlnrpfFXc a anrp  
 122 1 2212121111 1 4:21  
 // // // // // // /  
 481 AACATACAGGGGGGGAAGACCTCTCCGTGCTCTACCTCGAGCTCCAGGATAGTGGCACC 540  
 TTGTATGTCCCCCTCTCTGGGAGGACAGAGTTCGACCTCGAGGTCTTATCACCCTGG  
 AsnIleGlnGlyGlyLysThrLeuSerValSerGlnLeuGluLeuGlnAspSerGlyThr -

N N N  
 Na b b  
 lp o o  
 aH 2  
 31 1  
 /  
 541 TCGACATGCACTGTCTTCCAGAACCAAGAAGGTGGAGTTCAAAATAGACATCGTGGTG 600  
 ACCGTGACGTGACAGAACGTCTCTGGTCTCTTCCACCTCAAGTTTATCTGTAGCACCAC  
 TrpThrCysThrValLeuGlnAsnGlnLysLysValGluPheLysIleAspIleValVal -

M A HS M M  
 a l ac n n  
 e u eu 1 1  
 1 1 31 1 1  
 /  
 601 CTAGCTTTCCAGAAGGCTCCACCATAGTCTATAAGAAAGAGCGGGGAACAGGTGGAGTTC 660  
 GATCGAAAGGTCTTCCGGAGGTCTATCAGATATCTTCTTCCCCCTTGTCCACCTCAAG  
 LeuAlaPheGlnLysAlaSerSerIleValTyrLysLysGluGlyGluGlnValGluPhe -

A A M  
 l l n  
 u u 1  
 1 1 1  
 /  
 661 TCCTTCCCACTCCCTTTACAGTTGAAAAGCTGACGGCCAGTGGCGAGCTGTGGTGGCAG 720  
 AGGAAGGCTGAGCGGAATGTCAACTTTTCGACTGCCCTACCGCTCGACACCACCGTC  
 SerPheProLeuAlaPheThrValGluLysLeuThrGlySerGlyGluLeuTrpTrpGln -

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## FIG. 11(cont'd)

		P	S	
	MH	M2	MNDa	
	np	nl	bdpu	
	lh	lm	oen3	
	11	11	121A	
		/	/	

721 CCGGAGAGGGCTTCTCTCTCCAGTCTTGGATCACCTTTGACCTGAAGAACAAGGAAGTC 790

-----

CCCTCTCTCCGAAGGAGGAGGTTCAACCTAGTGGAAACTGGACTCTCTGTTCTCTTAC

AlaGluArgAlaSerSerSerLysSerTrpIleThrPheAspLeuLysAsnLysGluVal -

	S	BZS	P	S		
	AM	scC	ADNpPDaS	A		
	ca	cor	vrllusui	1		
	Ze	NRP	aaaMse9n	u		
	23	121	22411161	1		
		/	/	/	/	/

781 TCTGTAAACGGGTTACCCAGGACCCTAAGCTCCAGATGGGCAAGAAGCTCCCGCTCCAC 840

-----

AGACATTTTCCCAATGGGTCTCTGGCATTCGAGGCTACCCGTTCTTCGAGCGCGAGGTC

SerValLysArgValThrGlnAspProLysLeuGlnMetGlyLysLysLeuProLeuHis -

	BZS						BZS	S
	M	scC	HS	D	M	H	scC	MHa
	n	cor	at	d	n	p	cor	rau
	1	NRP	eu	e	1	h	NRP	1e9
	1	121	31	1	1	1	121	136
		/	/				/	/

841 CTCACCTGCCCCAGCCCTTGCTCAGTATGCTGGCTCTGGAAACCTCACCTGCCCCCTT 900

-----

GAGTGGGACGGGGTCCCGAACCTAGTCATACGACCCAGACCTTTGGAATCCGACCGGGAA

LeuThrLeuProGlnAlaLeuProGlnTyrAlaGlySerGlyAsnLeuThrLeuAlaLeu -

		S	BZS					
		f	scC					
		a	cor					
		M	NRP					
		1	121					
			/					

901 GAAGCGAAACAGGAAGTTGCATCAGGAAGTGAACCTGGTGGTATGAGAGCCACTCAG 960

-----

CTTCGCTTTTGTCTTTCAACGTAGTCCTTCACTTGGACCACCACCTACTCTCGGTGAGTC

GluAlaLysThrGlyLysLeuHisGlnGluValAsnLeuValValMetArgAlaThrGln -

			P	S	S			
			ADNpPDaS	f	D	MA		
			vrllusui	a	d	nl		
			aaaMse9n	N	e	lu		
			22411161	1	1	11		
			/					

961 CTCCAGAAAAATTTCACCTGTGAGGTGTGGGACCCACCTCCCTAAGCTGATGCTGAGT 1020

-----

GAGGTCTTTTAACTGGACACTCCACACCCCTGGGTGGAGGGGATTGCACTACCACTCA

LeuGlnLysAsnLeuThrCysGluValTrpGlyProThrSerProLysLeuMetLeuSer -

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		M						
		n						
		1						
		1						

1021 TTGAACCTGGAGAACCAAGGAGCCAAAGTCTCGAAGCGGGAGAACCGGCTGTGGGTGCTG 1080

-----

AACTTTGACCTCTTGTTCTCTCCGTTTCCAGAGCTTCGCCCTCTTCCGCCACACCCACGAC

LeuLysLeuGluAsnLysGluAlaLysValSerLysArgGluLysAlaValTrpValLeu -

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*FIG. 11(cont'd)*

DM	P	D	M	H	P S	H
ds	o	d	n	1 A	ADpPeS	1
et	k	e	e	n v	vtusui	n
12	1	1	3	f a	aaMs9n	f
/				1 1	221161	1
					// //	

1081 AACCCTGAGGCGGGGATGTGGCAGTGTCTGCTGAGTGAAGTCCGGACAGGTCCCTGCTGGAA 1140  
-----+-----+-----+-----+-----+-----+-----+-----+  
TTGGGACTCCGCCCTACACCGTCACAGACGACTCACTGAGCCCTGTCTCAGGACGACCTT  
AsnProGlnAlaGlyMetTrpGlnCysLeuLeuSerAspSerGlyGlnValLeuLeuGln -

H	S	P	S	P
NSALT	RDNC	n	BMDNAX	TP
lacna	pact	u	bbspduh	us
alccq	apif	4	vozejo	4t
31121	2111	H	1112A3	H1

1141 ~~TCACATCAAGCTCTGCCCATGCTGACCCCGGTGCAGCCCATGTCAGATCTTCCA~~ 1200  
~~AGGCTGTAGCTCCAGACGGGTGTACCAGCTGGGCCCACGTCGGTACACTCTAGGACGT~~  
 SerAsnIleLysValLeuProThrTrpSerThrProValGlnProMet~~Trp~~AspPheAla -  
STOP

		P S	P S	
A	MB	ADNnpMPaS	ADNpPaS	WYDax
1	nb	vrllluasi	vrllusi	bcpub
u	lv	aaaaMaa9n	aaaMa9n	oenjo
1	11	224411161	2241161	:21A2

1201 CCCCAGCTTGGGACCC AGAGGTC CCCTTAA CTTCAAT CGGAGATCCCA TTCT  
 -----  
 CCGGTCGAACCCCTGGGATCTCAGGGGAAAAATAAACCTAACCTCTAGGGTAAGA 1260  
 AlaGlnLeuGlyAspProArgGlyProLeuPheTyrPheGluLeuGlyAspProAlaSer -

N	A	Clas	MON	A
1	1	14	14h	1
2	1	14	14h	1
3	1	14	14h	1

1261 CATGTTTGACAGCTATCATCGATAAGCTAGCTTTAATCGCGTAGTTTATCAGTAAA 1320  
-----  
GTACAAACTGTGGAATAGTAGCTATTCGATCGAAATTACGCCATCAAAAGTGTCAATT  
HisValEndGlnLeuIleIleAspLysLeuAlaLeuMetArgEndPheIleThrValLys -

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B N  
a l  
n a  
l 4

P R H  
o k i n  
k e n P b  
l l l a  
l l l

H B  
P a  
H B  
l l

T T G C T A A C G C A G T A G G C A C C G T G T A T G A A A T C T A A C A A T G C C C T C A T C G T C A T C T C T G G  
 :32: ----- 1380  
 A A C G A T T G C C G T A G T C C G T G G C A C A T A C T T T A G A T T G T T A C G C C A G T A G C A G T A G C A G C C  
 L e u L e u T h r G l n S e r G l y T h r V a l T y r G l u I l e E n d G l n C y s A l a H i s A r g H i s P r o L a g -

N	S	BES				S S
1	MMf	SCC	P	HM	R	MMNaHC
2	ANA	COF		ps	s	pscuar
3	eln	NRP	K	ap	a	api9eP
4	311	121	1	21	1	211631
	//	/		/		// //

3785 1381  
-----  
GTGGCAGTGGGACCTACGACATCCGTATCCGAACCAATACGGCCATGACGGCCCCGGAGAA 1440  
HisArgHisProGlyCysCysArgHisArgLeuGlyTyrAlaGlyThrAlaGlyProLeu -

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## FIG. 11(cont'd)

M	E		S		P	K	S	
n	c		MBf		n	NH	i	NH2
1	R		aba		u	ba	n	baa
1	V		evN		4	ee	P	aeN
			311		8	11	1	121

1441 GCGGGATATCGTCCATTCCGACAGCATCGCCAGTCACTATGCGGTGCTGCTAGCCGTATA 1500  
 -----  
 CGCCCTATAGCAGGTAAGGCTGTGCTAGCCGTCAGTGATACCGCAGCAGCATCGCGATAT  
 AlaGlyTyrArgProPheArgGlnHisArgGlnSerLeuTrpArgAlaAlaSerAlaIle -

H		BH		P	
1PHM		scN		C	Hn
nshs		pls		f	au
Ppat		lap		r	ea
1111		212		1	1H

1501 TCGGTTGATGCAATTTCATGCGGACCCGTTCTCGGAGCACTGTCCGACCCGCTTTGCCCG 1560  
 -----  
 ACCCAACTACGTTAAAGATACCGCTCGGCAAGAGCCCTCGTGACAGGCTGCCCAACCTGCC  
 CysValAspAlaIleSerMetArgThrArgSerArgSerThrValArgProLeuTrpPro -

P		N	T	P	S	N
n		1	a	nMDaT		1
4		a	q	ubdpuh		a
H		4	1	DoenJa		3
				2121A1		

1561 CCGCCCACTGCTGCTGCGTTTCCTACTTCGAGCCCACTATCCACTACCGCATCATGCCGAC 1620  
 -----  
 CGCCCGTCAAGACCGAGCCGAGCGATGAACCTCGGTGATACCTGATCCGCTAGTACCGCTG  
 ProProSerProAlaArgPheAlaThrTrpSerHisTyrArgLeuArgAspHisGlyAsp -

H		NH		S		H	H
1		ps		CHHHHMHf		HMBAGHBHIN	
n		ap		fgappsa		psahihbana	
2		21		raeahpeN		apnaDaeePr	
1				11321111		2112111211	

1621 CACACCCGTCCTGTGCAATCTCTACGCCCGGACCCATCGTGGCCCGGCATCACCCGCCCCAC 1680  
 -----  
 GTGTGGGCAGGACACCTAAGAGATCGGCCCTCGGTAGCACCGCCCGTAGTGGCCCGCGGT  
 HisThrArgProValAspSerLeuArgArgThrHisArgGlyArgHisHisArgArgHis -

S		H	H		S	B
N2		2AGHBHIN	H		MNDa	3BMH
1a		ahihbanal	p		bdpu	apbs
an		naDaeePTa	h		oen3	alop
41		121112114	1		121A	2222

1681 AGGTCCCGTTGCTGCGCCCTATATCGCCGACATCACCGATCGCGAAGATCGCCCTCGCCA 1740  
 -----  
 TCACGCCAAGCAGCCCGGATATAGCCGCTGTAGTGGCTACCCCTTCTAGCCCGAGCGGT  
 ArgCysGlyCysTrpArgLeuTyrArgArgHisHisArgTrpGlyArgSerGlySerPro -

B	H		S		S		
BaN	N	1	NH		C	NH2NC	
aps	1	n	ba		f	apcr	
nlp	a	P	ae		r	eePiP	
222	3	1	12		23416	1	32111

1741 CTTCGGGCTCATGAGCGCTTGTTCGGCGTGGGTATCGTGGCAGGCCCCCGTGGCCCGGGG 1800  
 -----  
 GAAGCCCGAGTACTCGCGAACAAAGCCGACCCATACCAACCGTCCGGGGCAGCCGCCCCC  
 LeuArgAlaHisGlnArgLeuPheArgArgGlyTyrGlyGlyArgProArgGlyArgGly -

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## FIG. 11(cont'd)

	H	H		P		BH	
	BAQHBBHINN			u	u	sqN	H
	ahihbanal			u	u	pis	a
	naDaseePra			4	4	lap	e
	121112114			H	H	212	3
	/	////				//	

1801 ACTGTTGGCGCCATCTCTTCACGCACCAATTCCTTCGCGCGCGCGTGCCTCAACGGCCT 1860  
 -----  
 TCACAACCCCGCGGTAGAGGAACGTGCGTGGTAAGGAACCCCGCCCGCCACGAGTTGCCGGA  
 ThrValGlyArgHisLeuLeuAlaArgThrIleProCysGlyGlyGlyAlaGlnArgPro -

	B	M	P		H		S
	b	n	u		n		f
	v	l	4		g		a
	l	l	H		l		M
							l

1861 CAACCTACTACTGGCTGCTTCTTAATGCAGGAGTCCGATAAGCGAGAGCGTCTCTCCGAT 1920  
 -----  
 GTTCGATCATCAGCCGACCAAGCATTACGTCTCAGCGTATTCCCTCTCCGACGAGGCTA  
 GlnProThrThrGlyLeuLeuProAsnAlaGlyValAlaEndGlyArgAlaSerSerAsp -

	A	HM	H P		N
	l	ps	i nHT		l
	u	ap	n uhh		a
	l	21	P Das		3
			1 211		
			//		

1921 CCGCTTCAGAGCCCTTCAACCCAGTCAGCTCTCTCCGTCGCGCGCGCGCATGACTATCGT 1980  
 -----  
 CCGGAATCTCTCGGAAGTTGGCTCAGTCCAGCAAGCCCGCCCGCGCGCTACTGATAGCA  
 AlaLeuGluSerLeuGlnProSerGlnLeuLeuProValGlyAlaGlyHisAspTyrArg -

	P		M		N		F H
	n		b		a		B N HM n i HH
	u		o		a		a l psa u n ba
	4		2		a		n a spe 4 P ae
	H				3		1 4 211 H 1 12
							//

1981 CCGCGCACTTATGACTGTCTCTTATCATGCAACTCGTAGGACAGGTGCCGGCAGCCCT 2040  
 -----  
 CCGCGCTGAATACTGACAGAAGAAATAGTATGTTGAGCATCTGTCCACGGCCCGTCCCGA  
 ArgArgThrTyrAspCysLeuLeuTyrHisAlaThrArgArgThrGlyAlaGlySerAla -

	BH		S		H P		S
	bn		AsS		l nHT		HNDS
	vl		vul		n uhh		bdpu
	ll		a9n		P Das		oen3
			261		1 211		121A
							3
			//		//		//

2041 CTGGGTCAATTTTCGGCCAGGACCCCTTCCTCGAGCGCGACGATGATCGGCCTGTCCCT 2100  
 -----  
 GACCCAGTAAAGCCCGCTCTCTGCCGAAGCGACCTCCCGCTGCTACTAGCCCGACAGCGA  
 LeuGlyHisPheArgArgGlyProLeuSerLeuGluArgAspAspArgProValAla -

	H				S
	l				AsNS
	n		M	M	vuli
	f		l	a	a9an
	l		1	3	2641
					//

37872101 TCGGGTATTTCGGAATCTTCACGCCCTCGCTCAAGCCTTCGTGACTGGTCCCGCCACCAA 2160  
 -----  
 ACCCCATAAGCCTTAGAACGTGCGCGAGCGAGTTCCGAAGCAGTGACCAGCGCGGTGCTT  
 CysGlyIleArgAsnLeuAlaArgProArgSerSerLeuArgHisTyrSerArgHisGln -

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## FIC. 11(cont'd)

M		H		HMN	B N	CEAK	PH		H	M
a		a		psa	g	1 fauam	unhh	g	a	
e		e		ape	1	a rg4ea	DPaa	a	e	
2		3		211	1	3 11H33	2111	1	2	
				//		////	/			

ACGTTTCGGCGAGAAGCAGGCCATTATCGCCCGCATCGCCCGCGACCGCTCGGCTACGT  
 2261 TCCAAAGCCGCTCTTCGTCCGGTAATAGCGCCCGTACCGCCCGCTCGCCGACCCGATGCA 2220  
 ThrPheArgArgGluAlaGlyHisTyrArgArgHisGlyGlyArgArgAlaGlyLeuArg -

	F	F				H		
M	NT	NT	H	H	FM	1		H
n	urh	uh	g	a	ob	2		P
1	Dua	Da	a	e	ko	2		a
1	211	21	1	3	12	1		2

CTTGCTCGCGCTTCGGACCGCGAGGCTGGATCGCCCTTCCCATTTATGATCTCTCGCTTC  
 2221 GAACGACCCCAAGCCCTCGGCTCGGACCTACCGGAAGCGGTAATACTAAGAAGACCCGAAG 2280  
 LeuAlaGlyValArgAspAlaArgLeuAspGlyLeuProHisTyrAspSerSerArgPhe -

SP	S	F		B	BZS
M f2	f	NT	F	H	SH
s au	a	uh	o	a	pl
P N4	N	Da	k	e	Ma
1 1H	1	21	1	3	13
					121

CGCCCGCATCGCGATCGCCCGCTTCAGCCCATGCTCTTCAGCCAGCTAGATCAGGACCA  
 2281 CGCCCGCTAGCCCTACGGGGCGCAACGTCGGTACGACAGGTCGGTCCATCTACTCTCGT 2340  
 ArgArgHisArgAspAlaArgValAlaGlyHisAlaValGlnAlaGlyArgGlnArgPro -

	S	FP		S	S
A	MDa	NT		MDa	AsS
1	bcpu	uh		abcpu	vui
u	oen3	D4a		qoen3	a9n
1	121A	2H1		1121A	261

TCAGCGACAGCTTCAGGATCGCTCGCCCGCTCTTACCAGCCTAACTTCGATCTACTGACC  
 2341 AGTCCCTGTGGAAGTTCTTAGCGAGCGCCGACAATCGTCCGATTGAAGCTAGTGACCTGG 2400  
 SerGlyThrAlaSerArgIleAlaArgGlySerTyrGlnProAsnPheAspHisTyrThr -

N	S		F		BH		
s MDaM			n	B	M	sqm	M
p bcpu			u	g	n	pis	1
B oen3e			4	1	1	lap	a
2 121A3			H	1	1	212	3

GCTGATCGTACCGCGATTATGCGCCCTCGCCGAGCACATCGGAACGGGTTGGCATGGAT  
 2401 CGACTAGCAGTGGCGCTAAATACGGCGGAGCCCGCTCGTGTACCTTGCCCAACCGTACCTA 2460  
 AlaAspArgHisGlyAspLeuCysArgLeuGlyGluHisMetGluArgValGlyMetAsp -

H	F	H		F		F	
BAQHBNHINN			H	NTM	NT	N N	HMN
abihbuanal			g	uhn	uh	1	1
baDae4ePra			a	Dal	Da	a	a
12111H2114			1	211	21	3	4

TGTAGCGCGCCCGCTATACCTTGTCTGCGCTCGCCCGCTTCGGTTCGGTTCGATGGAGCCG  
 2461 ACATCCCGCGCGGATATGGAACAGACGGAGGGCGCAACGCAGCGCCACGTACCTCGGC 2520  
 CysArgArgArgProIleProCysArgProArgValAlaSerArgCysMetGluPro -

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## FIG. 11(cont'd)

S S P H  
 aRc T M HON nb N H M I  
 uar a n psa ua l p n n  
 9eP q l ape 4n a h l f  
 631 l l 211 H1 4 l l l  
 // //

2521 CCCCACCTCGACCTGAATGGAAGCCGGCCGACCTCGCTAACGGATTACCACTCCAAGA 2580  
 CCGGTGGAGCTGGACTTACCTTCGGCCCGCGTCCAGCGGATTGCCTAAGTGGTGAGGTTCT

GlyHisLeuAspLeuAsnGlySerArgArgHisLeuAlaAsnGlyPheThrThrProArg -

P H P H  
 2 M 1P3HM Sf H  
 l l nshs cl q  
 M a Pmat yM a  
 l 4 llll ll l

2581 ATTGGAGCCAATCAATTCTTCGGGAGAACTGTGAATGCCCAAACCAACCTTCGCCAGAAC 2640  
 TAACCTCGGTAGTTAAGAAGCCCTCTTGACACTTACCGGTTTGGTTGGGAACCGTCTTC

IleGlyAlaAsnGlnPheLeuArgArgThrValAsnAlaGlnThrAsnProTrpGlnAsn -

P P P H S S  
 nT n n nnBITH A B f BMDNa A  
 ub u u uubnhh v b a cbpdu l  
 Da 4 4 D4vPaa a v M lone3 u  
 21 H H 2H1111 l l l 1112A l

2641 ATATCCATCGCGTCCGCCATCTCCAGCAGCCCGACCGCGCCATCTCGGGCGATCATCAG 2700  
 TATAGGTAGCCGAGCCCGTAGAGGTCTCGCGCTCCGCCCGTAGAGCCCCCTACTAGTC

IleSerIleAlaSerAlaIleSerSerSerArgThrArgArgIleSerGlyAspAspGln -

FN PFP H S  
 naPF ninHDT H H M NaaA HONC B  
 upvo unuhhnh p p n lupl pscr b  
 4Buk DPDeala h h l a4Hu apif v  
 H221 2121111 l l l 3H11 2111 l

2701 CTGCGCTCGCGCGTTTCGGTGATGACGGTGAACCTCTGCACACATCCAGGTCCCGGAGAC 2760  
 GACGGAGCGCGCAAGCCACTACTGCCACTTTTGCAGACTGTGTACGTCCAGGGCCTCTG

LeuProArgAlaPheArgEndEndArgEndLysProLeuThrHisAlaAlaProGlyAsp -

H A S S H P N  
 a l 2 HONC P i nHT a  
 e u N pscr o q n ubh p  
 3 l l 2111 k a P Daa B  
 2111 l l 1 211 2

2761 GGTACAGCTTGCTGTAAAGCGGATGCCGGGAGCAGACAAGCCCGTCAGGGCGCGTCAGC 2820  
 CCAGTGTCGAACAGACATTCCCTACGGCCCTCGTCTGTTCGGG-CAGTCCCGCGCAGTCC

GlyHisSerLeuSerValSerGlyCysArgGluGlnThrSerProSerGlyArgValSer -

H P N TBM M A  
 l Hn l tba a C  
 n bu A bve e C  
 P a4 3 113 2 C  
 l 1H

2821 CCGTGTTGGCGGGTGTCGGGGCGCAGCCATGACCCAGTCAAGTACCGATAGCGGAGTGTA 2880  
 CCCACAACCGCCCAAGCCCGCGTCCGTACTGGGTCAAGTGCATCGCTATCGCCCTCACAT

GlyCysTrpArgValSerGlyArgSerHisAspProValThrEndArgEndArgSerVal -

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## FIG. 11(cont'd)

	P	S	R D	A	BH
	D	S	S D	P	sgNN
	U	A	A D	A	plsd
	4	N	A D	L	lape
	H	1	1 1	1	2121

2881 TACTGGCTTAACTATGCGGCATCAGAGCAGATTCTACTGAGAGTGCACCATAATCGCGGTGT 2940  
 ATGACCGAATTGATACGCGGTAGTCTCGTCTAACATGACTCTCACGTGGTATACGCCACA  
 TyrTyrLeuAsnTyrAlaAlaSerGluGlnIleValLeuArgValHisHisMetArgCys -

S		H	S
f		1	EH2
A		b	n haa
N		o	P aen
1		2	1 121

2941 GAAATACCGCACAGATCGGTACGAGAGAAATACCGCATCAGCGCGCTCTTCGGCTTCCTCG 3000  
 CTTTATGCGCGTGTCTACCGATTCCGTCTTTTATGCGGTAGTCCCGCAGAACCGGAGCAGC  
 GluIleProHisArgCysValArgArgLysTyrArgIleArgArgSerSerAlaSerSer -

H	P H	P P	A
M 1	n 1 BH	n n	1
n n	u n bh	u u	1
1 2	4 P vs	4 4	1
1 1	H 1 11	H H	1

3001 CTEACTGACTCGCTCGGCTCGGTCTTCGGCTCGCGCGAGCGGTATCAGCTCACTCAAG 3060  
 GAGTCACTCAGCGACCGCAGCCAGCAACCGCAGCGCGCTCGCCATAGTTCAGTCACTTC  
 LeuThrAspSerLeuArgSerValValArgLeuArgArgAlaValSerAlaHisSerLys -

H	N
1	Ns
n	lp
2	ah
1	31

3061 CCGGTAATACGGTTATCCACAGAAATCAGCGGATAACCCAGCAAGAACATGTGAGCAAAA 3120  
 CGCCATTATGCCAATAGGTGTCTTAGTCCCTATTGCGTCTCTTCTGTACACTCGTCTT  
 AlaValIleArgLeuSerThrGluSerGlyAspAsnAlaGlyLysAsnMetEndAlaLys -

H	BE S	P P	N
a	schc M	HN nt	1
e	coar 1	au uh	4
3	NRaP a	e4 Da	4
	1234 4	3H 21	

3121 GCGCAGCAAAAGCCGAGGACCTTAAAAAGCGCGCGTTCCTGCGGTTTTTCCATAGGCTC 3180  
 CCGGTCTGTTTTCCGCTCCTTGGCATTTTCCGGCGCAACGACCGCAAAAGGTATCCGAG  
 GlyGlnGlnLysAlaArgAsnArgLysLysAlaAlaLeuLeuAlaPhePheHisArgLeu -

S	T	M	H
S	A	1	g
N	q	1	a
1	1	1	1

3181 CCGCGCGCGTGCAGCAGCATCAGCAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCGGACA 3240  
 CCGCGCGCGTGCAGTCTAGTGTCTTCTAGCTCCGAGTTCAGTCTCCACCGCTTTCGGCTGT  
 ArgProProAspGluHisHisLysArgArgArgSerSerGlnArgCTTAAACAsnProThr -

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FIG. 11'cont'd)

BES	BES	A	H
SCC	SCC	l	l HM
COF	COF	u	n hn
NRP	NRP	u	P al
121	121	1	1 11

3241 CCACTATAAAGATACCAGCGCTTCCCTCGGAAGCTCCCTCGTCCGCTCTCCTGTTCCG 3300  
 CCTGATATTTCTATGCTCCGCAAGCGGGACCTTCGACGGAGCACCGGAGAGGACAAGGC  
 GlyLeuEndArgTyrGlnAlaPheProProGlySerSerLeuValArgSerProValPro -

F	HM	H
n	ps	l HH
u	ap	n ha
4	21	P ae
H		1 12

3301 ACCCTCCCGCTTACCGGATACCTGTCCCGCTTCTCCCTTCGGGAAGCGTCCCGCTTCT 3360  
 TCGGACGGCGAATCGCCTATCGACAGCGGGAAGACGGAGCCCTTCGACCGCGGAAGA  
 ThrLeuProLeuThrGlyTyrLeuSerAlaPheLeuProSerGlySerValAlaLeuSer -

D	A
d	l
e	u
1	1

3361 CAATGCTACCGTGTAGGTATCTCAGTTCCGTGTAGGTCTGCTCCCTCCAAGCTGGGCTGT 3420  
 GTTACGAGTCCGACATCCATAGAGTCAAGCCACATCCACCAAGCCAGCTTCGACCGGACA  
 GlnCysSerArgCysArgTyrLeuSerSerValEndValValArgSerLysLeuGlyCys -

A	BH	B	NP	H	HM	H
P	sgn	b	sn	l H	HM	i
a	pis	b	pu	n h	psa	n
L	lap	v	B4	P a	ape	2
1	212	1	2H	1 1	213	1

3421 GTCCACGAACCCCCCGTTACCCCCGACCGCTCCCGCTTATCCGGTAACTATCGTCTTGAG 3480  
 CACGTGCTTCCGGGGCAAGTCCGGCTCGCCAGCGCGAATAGGCCATTGATAGCAGAACTC  
 ValHisGluProProValGlnProAspArgCysAlaLeuSerGlyAsnTyrArgLeuGlu -

S	F	F	BM	B	M
HMNe	n	n	ba	b	n
psct	u	u	ve	v	1
apiP	4	4	13	1	1
2111	H	H			

3481 TCCAAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGC 3540  
 ACGTTGGGCCATTCTGTGCTGAATAGCGGTGACCGTCTGTCGGTGACCATTCCTTAATCG  
 SerAsnProValArgHisAspLeuSerProLeuAlaAlaAlaThrGlyAsnArgIleSer -

H
a
e
3

3541 AGAGCGAGGTATGTAGCGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCCTAACTACGGCTAC 3600  
 TCTCGCTCCATACATCCGCCACGATGTCTCAAGAAGTTACCCACCGGATTGATGCCGATC  
 ArgAlaArgTyrValGlyGlyAlaThrGluPheLeuLysTyrTyrProAsnTyrGlyTyr -

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## FIG. 11(cont'd)

H H H  
 1 1 1  
 n b a  
 P a e  
 1 1 3  
 3601 ACTAGAAGGACAGTATTTGGTATCTCGGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGA 3660  
 TGATCTTCTCTGTCATAAACCATAGACCGGAGACGACTTCGGTCAATCGAAGCCCTTTCT  
 ThrArgArgThrValPheGlyIleCysLeuLeuLysProValThrPheGlyLysArg -  
 S  
 A MNDaM  
 1 bdpup  
 u oen3p  
 1 121A21  
 3661 GTTCGTAGCTCTTGATCCGGCAAAACCAACCCGCTGGTAGCGGTGGTTCCTTCG 3720  
 CAACCATCGAGAACTAGCGCGTTTGTTCGTGGCGACCATCGCCACCAAAAAACAAACG  
 ValGlySerSerEndSerGlyLysGlnThrThrAlaGlySerGlyGlyPhePheValCys -  
 F H S S S  
 n BnHIT MNDaX MNDaX MNDaX  
 u buhah bdpuh bdpuh bdpbu  
 4 vDaPa oen3o oen3o oen3o  
 H 12111 121A2 121A2 1212A  
 3721 AACCGCAGATTACCGGCAAAAAAGCATCTCAAGAGATCTTTCATCTCTTCTAGC 3780  
 TCGTCTCTAATCGCGCTCTTTTCTCTAGAGTTCTTCTAGGAACTAGAAAAGATCC  
 LysGlnGlnIleThrArgArgLysLysGlySerGlnGluAspProLeuIlePheSerThr -  
 D H M H H  
 d g a 1 b  
 e a e 3 o  
 1 1 2 3 2  
 3781 GGGTCTGACGCTCAGTCCGAACGAAACTCACGTTAAGCGATTTTGGTCATGAGATTATCA 3840  
 CCCAGACTCGGAGTCACCTTCGCTTTTCTAGTCCAATTCCTAAAAACAGTACTCTAATAGT  
 GlySerAspAlaGlnTrpAsnGluAsnSerArgEndGlyIleLeuValMetArgLeuSer -  
 S S S S A  
 H MNDaX M MNDaX BMDNaX MNDaX  
 p bdpuh a bdpuh gbpduh bdpu 1  
 b oen3o e oen3o lone3o oen3 u  
 1 121A2 1 121A2 2112A2 121A 1  
 3841 AAAAGGATCTTCACCTAGATCTTTTTCAGATCTCCCGATCTTTAGCTGCTTGGTTTGGC 3900  
 TTTTCTAGAACTGGATCTAGGAAAAGTCTAGAGGGCTAGAAATCGACAGAACCACCGG  
 LysArgIlePheThrEndIleLeuPheArgSerProAspLeuEndLeuSerTrpPheAla -  
 H H D MR  
 1 1 d ds  
 n h e la  
 P a 1 11  
 1 1  
 3901 CAAAGCGCATTCGATAATCTTTTCAGGGTTATGCGTTGTTCCATAACAACCTCTTAGTACA 3960  
 GTTTCGGCGTAACGTATTAGAAAGTCCCAATACCGCAACAAGGTATGTTGGAGGAATCATGT  
 GlnSerAlaLeuHisAsnLeuSerGlyLeuCysValValProTyrAsnLeuLeuSerThr -  
 3792

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## FIG. 11(cont'd)

N  
 NsH  
 lpp  
 aHh  
 311  
 /  
 M  
 n  
 l  
 l  
 H  
 i  
 n  
 c  
 2

1961 TCAACCATTTATCACCCTCAGAGGTAAAATAGTCAACACCCACCGTCTAGATAATTATC 4020  
 -----  
 ACGTTGGTAATAGTCCCGGTCTCCAATTTATCAGTTGTCCGTGCCCAATCTATAAATAG  
 CysAsnHisTyrHisArgGlnArgEndAsnSerGlnHisAlaArgCysEndIlePheIle -

HM BH M P  
 pa sqn n n A  
 he pis u l  
 12 lap 1 4 u  
 212 1 H 1  
 //

4021 CCTTCCGGTGATAGATTTAACGTATGACCACAAAAAGCAACCATTAACACAGACCACC 4080  
 -----  
 GGAACGCCACTATCTAAATTGCATACTCGTGTTTTCTTTGGTAAATCGCTCGCTCGCTCG  
 ProCysGlyAspArgPheAsnValEndAlaGlnLysArgAsnHisEndHisLysSerSer -

B M H  
 b a g  
 v e a  
 1 2 1

4081 TTGAGGACCCACGTCCCTTAAGCAATTTATCAAAAAAGCAAAATCAACTTGGCTTAT 4140  
 -----  
 AACTCCTCCGTCCAGCCGAATTTCTTAAATACTTTTCTTTTACTTGAACCGAATA  
 LeuArgThrHisValAlaLeuLysGlnPheMetLysLysArgLysMetAsnLeuAlaTyr -

BES H P  
 SCC i o  
 cor n k  
 NRP f l  
 121 1

4141 CCCAGCAATCTGTCCGACACAAGATGGGGATCCCCCAGTCAGCCGTTCGTGCTTTATTTA 4200  
 -----  
 CGGTCTTTAGACAGCGTCTGTTCTACCCCTACCCCGTCAGTCCCAACCAACGAAATAAAT  
 ProArgAsnLeuSerGlnThrArgTyrGlyTyrGlySerGlnAlaLeuValLeuTyrLeu -

S P  
 fN n  
 as u  
 H1 4  
 11 H

4201 ATGCCATCAATGCATTAAATGCTTATAACGGCCGCAATGCTTACAAAAATCTCAAAGTTA 4260  
 -----  
 TACCGTAGTTACGTAAATTACGAATATTCCGGCGTAACGAATGTTTTTAAGAGTTTCAAT  
 MetAlaSerMetHisEndMetLeuIleThrProHisCysLeuGlnLysPheSerLysLeu -

M  
 b  
 o  
 2

4261 CGGTTGAAGAAATTTAGCCCTTCAATGCCAGAGAAATCTACGAGATGTATGAAGCGGTTA 4320  
 -----  
 CGCAACTTCTTAAATCGGCAAGTTACCGGTCTCTTTAGATGCTCTACATACTTCCCAAT  
 AlaLeuLysAsnLeuAlaLeuGlnSerProGluLysSerThrArgCysMetLysArgLeu -

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## FIG. 11(cont'd)

P M D B R N  
 2 u a d b s l  
 4 e v 1  
 H 3 1 1 1 3  
 4321 GTATGCAGCCGTCACCTTAGAAGTGAGTATGAGTACCCTGTTTTCTCATGTCAGGCAG 4380  
 CATACGTCGGCAGTGAATCTTCACTCATCTCATCGGACAAAAAGAGTACAGTCCCTC  
 ValCysSerArgHisLeuGluValSerMetSerThrLeuPhePheLeuMetPheArgGln -

H DFI AD S H  
 P don ld 2 P  
 h ekd ue a h  
 1 113 11 1 1  
 4381 GGATGTTCTCACCCTAACCTTAGAACCTTACCAAGCTGATCGGCACAGATCGGTAACCA 4440  
 CCTACAGAGTGGATTGGAATCTTGGAAATGGTTTCACTACCCCTCTCTACCCATTGGT  
 GlyCysSerHisLeuSerLeuGluProLeuProLysValMetArgArgAspGlyEndAla -

H BM N  
 1 1 1  
 2 2 3  
 1 11  
 4441 CAACCAAAAAAGCCAGTCATTCTCCATTCTCGCTTCAGCTCAAGCTAATTCATGACCG 4500  
 GTTCGTTTTTTTCGGTCACTAAGAGCTAAGACCGTACTCCAATCTCCATTAGGTAATCGG  
 GlnProLysLysProValIleLeuHisSerGlyLeuArgLeuLysValIleProEndPro -

H H D  
 1 1 1  
 1 2 1  
 4 3 1  
 4501 CACCAACAGGCTCCAAGCCAGCTTCTCAGCGGAATGTTAATTCTCGTTGACCCTGAGC 4560  
 GTGGTTGTCCGAGGTTCCGTCGAAAGCACTGCCCTTACAATTAAGAGCAACTGGGACTCG  
 HisGlnGlnAlaProSerGlnAlaPheLeuThrGluCysEndPheSerLeuThrLeuSer -

S H H  
 SCC P P  
 cor h h  
 NRP 1 1  
 121  
 4561 AGGCTGTTGAGCCAGGTGATTTCTGCATAGCCAGACTTGGGGGTGATGAGTTTACCTTCA 4620  
 TCCGACAACTCGGTCCACTAAAGACGTATCGGTCTGAACCCCACTACTCAAAATGGAAAT  
 ArgLeuLeuSerGlnValIleSerAlaEndProAspLeuGlyValMetSerLeuProSer -

R  
 1  
 1  
 1  
 3794 4621 AGAAACTAATTAGGGATAGCGGTGAGGTGTTTTTACAACCACTAAACCCACAGTACCCAA 4680  
 TCTTTCATTAAATCCCTATCGCCAGTCCACAAAAATGTTGGTCAATTTGGGTGTCATGGSTT  
 ArgAsnEndLeuGlyIleAlaValLeuPhePhePheAsnHisEndThrHisSerThrGln -

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## FIG. 11(cont'd)

S	N		M	H
MDa	1		a	a
bdpu	1		e	e
oen3	3		1	3
121A				
/ /				

4681 TGATCCCATGCAATGAGAGTTGTTCCGTTGTGGGAAAGTTATCGCTAGTCAGTGGCTG 4740  
 -----  
 ACTAGCGGTACGTTACTCTCAACAAGCCACACCCCTTCAATAGCGATCAGTCACCGGAC  
 -----  
 EndSerHisAlaMetArgValValProLeuTyrGlyLysLeuSerLeuValSerGlyLeu -

M	M	S	H	A	M
a	b	MDa	1	1	b
e	o	bdpu	n	h	o
2	2	oen3	p	a	2
		121A	1	1	
/ /					

4741 AACAGACGTTTCGCTGATCGGCAAGGTGTTCTCGTGGCGCCATAGCTGATAACAATTGAG 4800  
 -----  
 TCTCTGCAAAACCGACTAGCCGTTCCACAAGACCAGCCCGGTATCGACTATTGTTAACTC  
 -----  
 LysArgArgLeuAlaAspArgGlnGlyValLeuValGlyAlaEndLeuIleThrIleGlu -

H	PS	P	BM	HM	S
1B	rf	rdp	bn	ps	MDaX
nb	ua	ugs	vl	sp	pbdpub
fv	4N	4at	11	21	oen3o
11	H1	H11			1121A2
/ /	/ /	/ /	/ /	/ /	/ /

4801 CAAGAACTTTCATCCCGGCTTCAGCCCAAGCATCGCTCCCGGCTAGAGCATCTCTACCTA 4860  
 -----  
 GTTCTTAGAAGTAGCCCGGAGCTCGGGTCTACCGAGCCCGCATCTCTAGAGAGTGGAT  
 -----  
 GlnGluSerSerSerGlyLeuGlnProThrMetArgProAlaEndArgIleSerHisLeu -  
 4861 CCAACAATGCCCCCTGCAAAAAATAAATTCATATAAAAAACATACAGATAACCATCTG 4920  
 -----  
 CGTTTGTTACGGGGGACGTTTTTATTTAAGTATAATTTGTAATGCTATTGGTAGAC  
 -----  
 ProAsnAsnAlaProLeuGlnLysIleAsnSerTyrLysLysHisThrAspAsnHisLeu -

H	H	BH
p	i	d
b	n	e
1	2	1
		121
/		/

4921 CGGTGATAAAATTATCTCTGGCGGTGTTGACATAAATACCACTGGCGGTGATACTGAGCAC 4980  
 -----  
 GCCACTATTTAATAGAGACCGCCACAACCTGTATTTATGGTGACCGCCACTATGACTCGTG  
 -----  
 ArgEndEndIleIleSerGlyGlyValAspIleAsnThrThrGlyGlyAspThrGluHis -

N	H	N	M	HH
a	g	1	a	GP
p	a	a	e	ah
2	1	3	3	11
/	/	/	/	/

3795 4981 ATCAGCAGGACGCCACTGACCACCATGAAGGTGACGCTCTTAAAAATTAAGCCCTGAAGAAG 5040  
 -----  
 TAGTCGTCTCTCGGTGACTGGTGGTCTTCACTCCGAGAAATTTAAATTCGGGACTCTCTC

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## FIG. 11(cont'd)

7  
 a BM                      B  
 u sb                      b  
 4 no                      v  
 H 12                      l  
 3041 CCCACCATTCAAAGCAGAGGCTTTGGGGTGTGTGATACGAAACGAACCAT 5092  
 -----  
 CCGTCGTAACTTTCGTCTTCCGAAACCCACACACTATCGTTTCTTCTGTA

GlySerIleGlnSerArgArgLeuTTPGlyValEndTyrGluThrLysHis??? -

## Enzymes that do cut:

AccI	Aha2	Afl2	AluI	ApaLI	AvaI	Ava2	BanI	Ban2	BbeI	BbvI
BclI	BglI	Bgl2	BamI	BspI2	BspMI	BstE2	BstNI	BstXI	CfrI	ClaI
DdeI	DpnI	Dra2	EagI	EcoB	EcoK	EcoRI	EcoR2	EcoRV	PvuD2	Pvu4H
FokI	PspI	Hae2	Hae3	HgaI	HgiAI	HgiDI	HhaI	Hinc2	Hind3	HinfI
HinPI	Hpa2	HphI	HaeI	Hae2	Hae3	HboI	Hbo2	HnlI	HspI	HstI
Hst2	HaeI	HarI	HclI	HdeI	Hde2	HheI	Hla3	Hla4	HruI	HsiI
Hsp2	HspB2	HspH1	PflMI	PpuMI	PsaI	PstI	Pvu2	RsaI	SacI	Sall
Sau3A	Sau96	SbfPI	SfaNI	SinI	SstI	StuI	StyI	TaqI	ThaI	TclI
Xho2	Xma3									

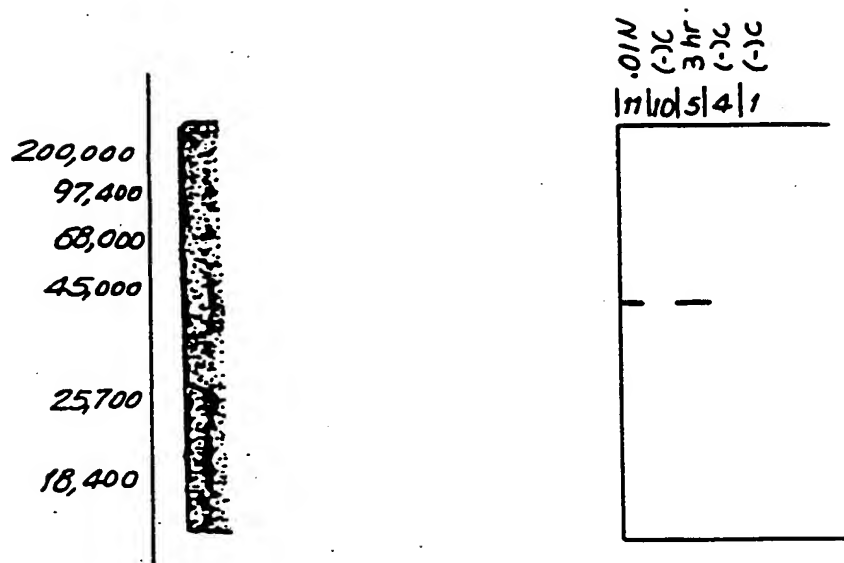
## Enzymes that do not cut:

Aat2	Aha3	Apal	Asp70	Asp71	Asu2	Avr2	BalI	BamHI	BspM2	BssH2
DraI	Dra3	EspI	HpaI	KpnI	MluI	NcoI	NotI	PaeR7	PvuI	Rsa2
Sac2	Scal	Sfil	SmaI	SnaBI	SpeI	SphI	SspI	Set2	XbaI	XhoI
XmaI	XmnI	Xor2								



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FIG. 12



lane 1 = Pre-induced

lane 4 = Uninduced

lane 5 = 3 hr. post-induction

lane 11 = overnight post-induction (~16 hr)

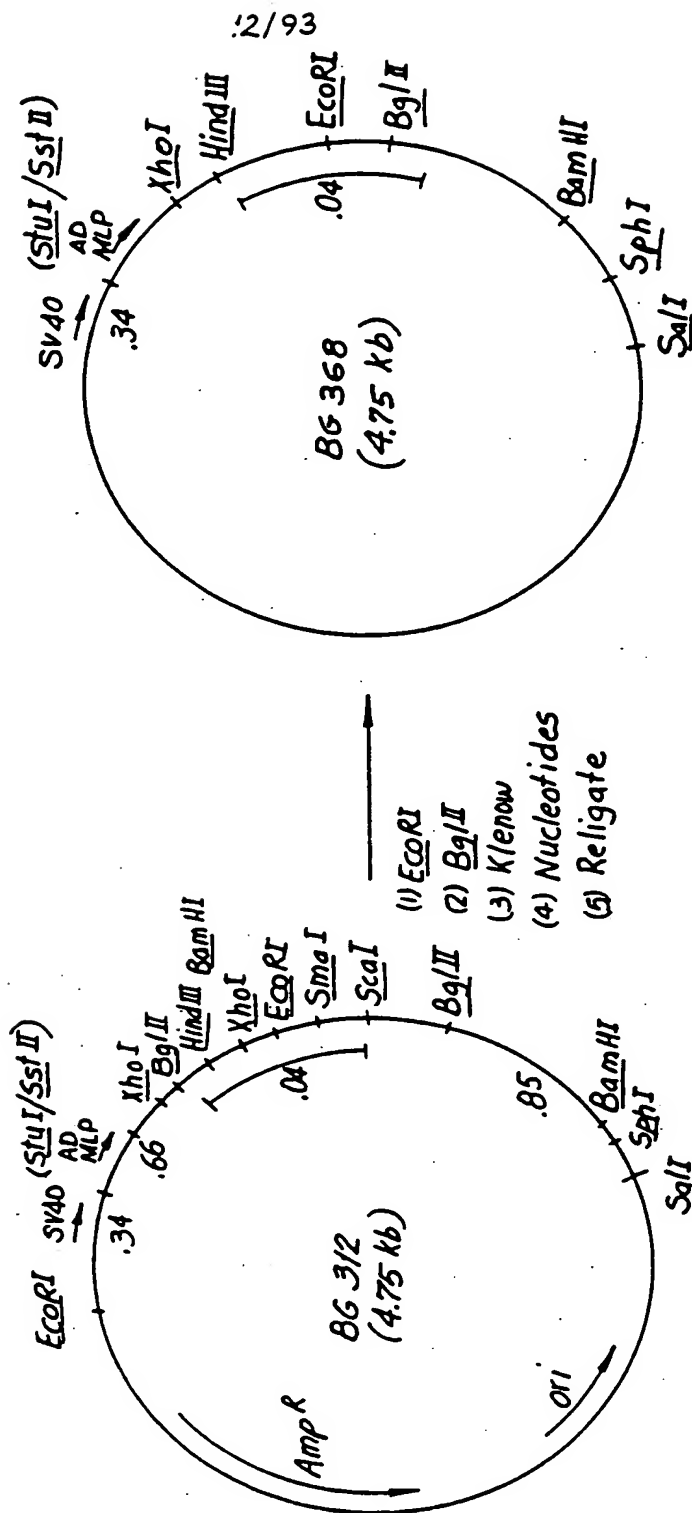
MW = Molecular wt. markers

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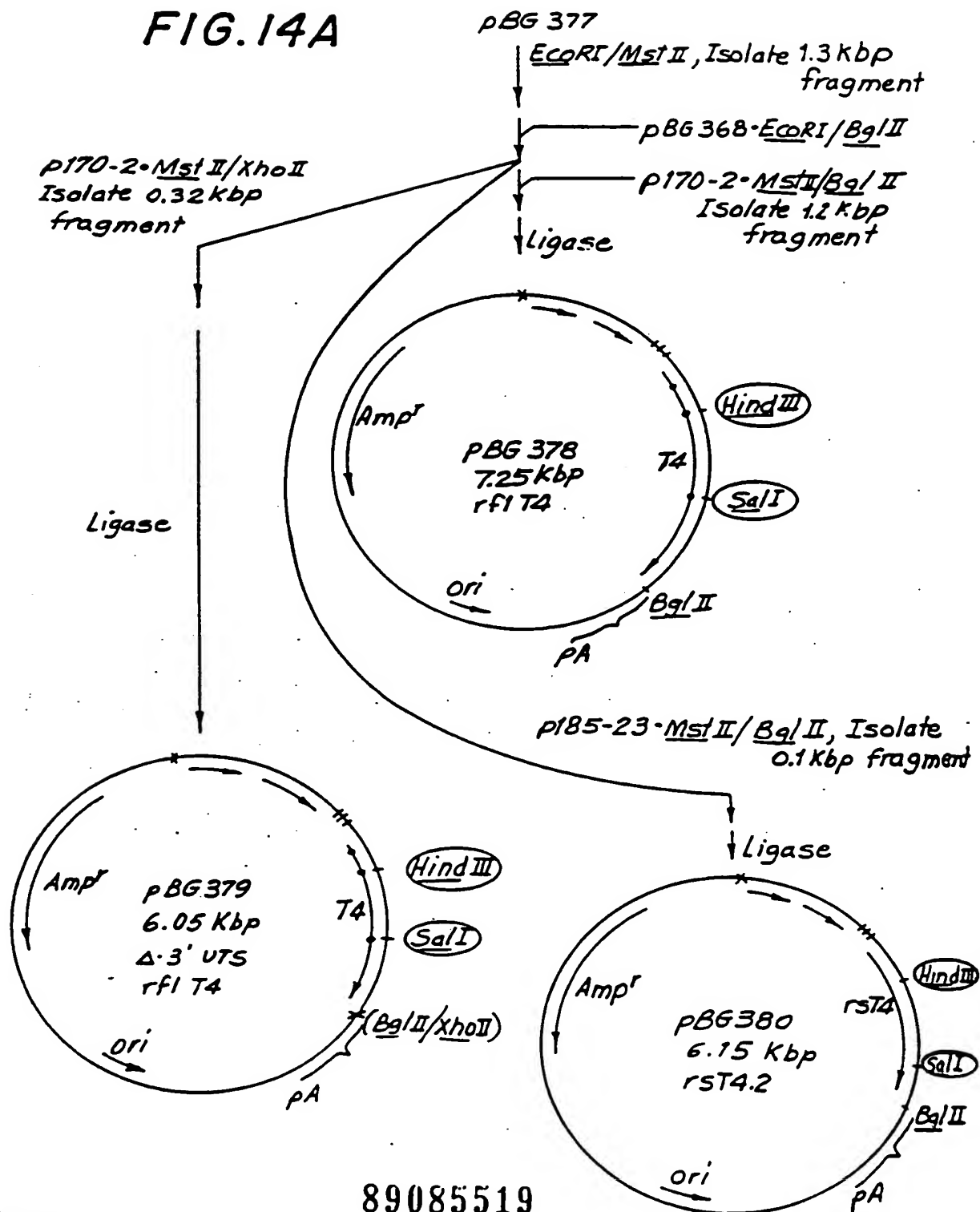
SUBSTITUTE SHEET

FIG. 13



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FIG. 14A

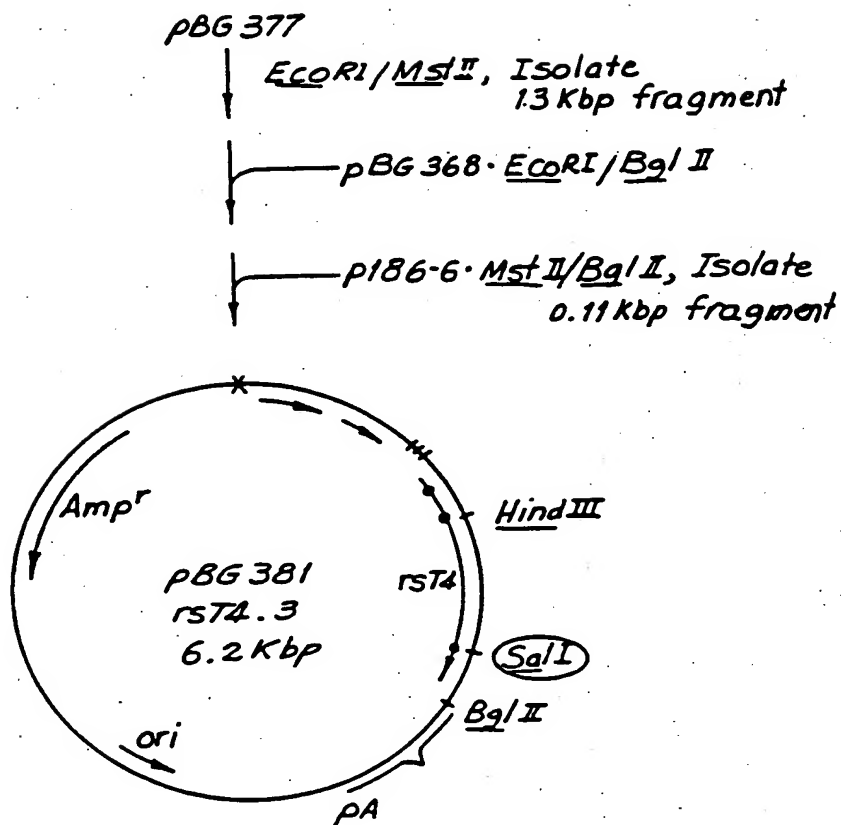


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# FIG. 14B



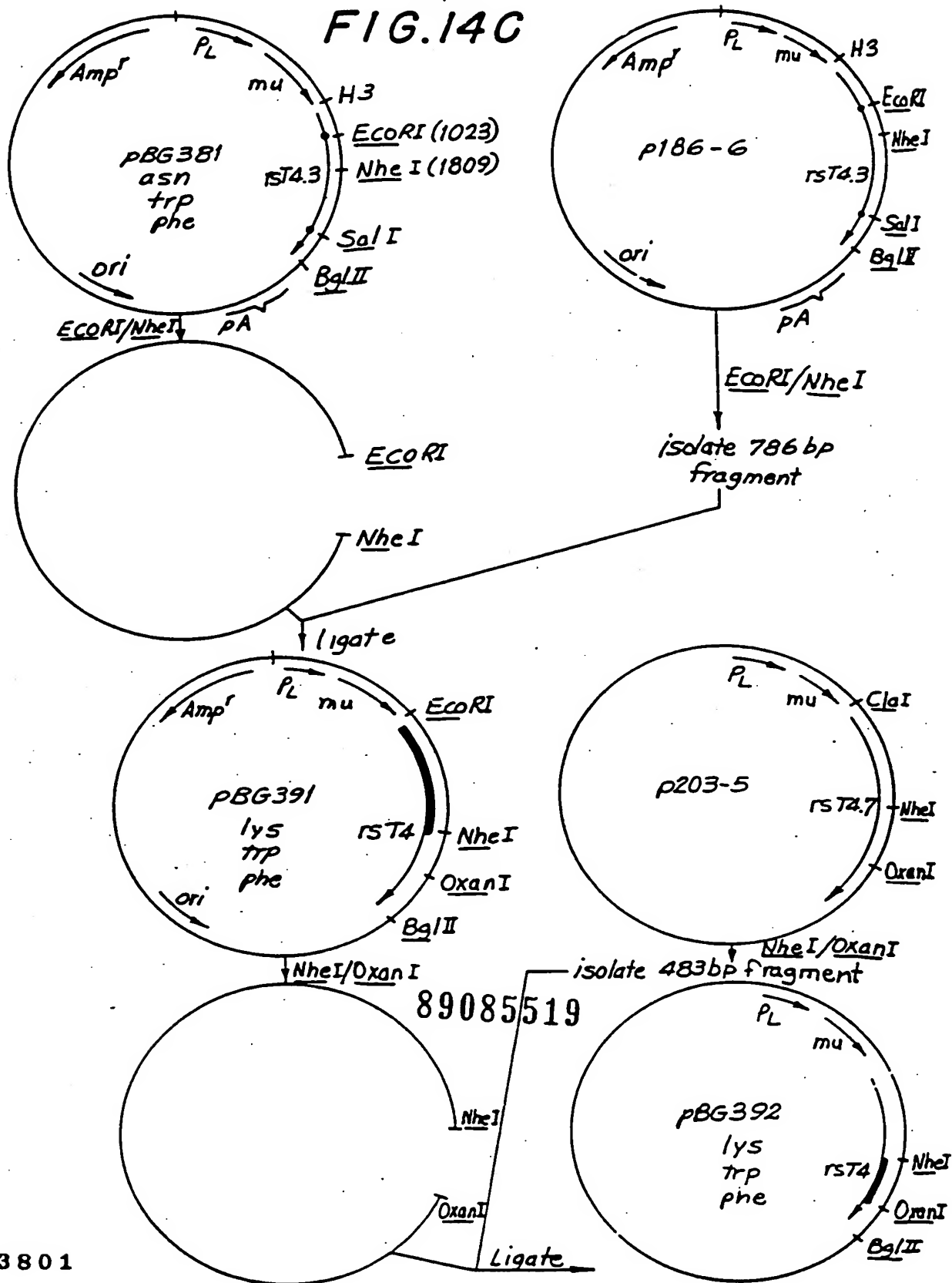
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FIG. 14C



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PBG391  
:BG368 backbone  
:soluble T4#3  
:AA #3 = LYS

*FIG. 15*

bg381.seq Length: 6151

1 GAATTAATTC CAGCTTGCTG TGGAAATGTGT GTCAGTTAGG GTGTGGAAAG  
51 TCCCCAGGCT CCCCAGCAGG CAGAAGTATG CAAAGCATGC ATCTCAATTA  
101 GTCAGCAACC AGGTGTGGAA AGTCCCCAGG CTCCCCAGCA GGCAGAAGTA  
151 TGCAAAGCAT GCATCTCAAT TAGTCAGCAA CCATAGTCCC GCCCCTAACT  
201 CCGCCCATCC CGCCCTAAC TCCGCCCAGT TCCGCCCAT TCTCCGCCCA  
251 TGGCTGACTA ATTTTTTTTA TTTATGCAGA GGCCGAGGCC GCCTCGGCC  
301 CTGAGCTATT CCAGAAGTAG TGAGGAGGCT TTTTGGAGG GGTCTCTCTC  
351 GTATAGAAAC TCGGACCACT CTGAGACGAA GGCTCGCGTC CAGGCCAGCA  
401 CGAAGGAGGC TAAGTGGGAG GGGTAGCGGT CGTTGTCCAC TAGGGGGTCC  
451 ACTCGCTCCA GGGTGTGAAG ACACATGTCT CCCTCTTCGG CATCAAGGAA  
501 GGTGATTGGT TTATAGGTGT AGGCCACGTG ACCGGGTGTT CCTGAAGGGG  
551 GGCTATAAAA GGGGGTGGGG GCGCGTTCGT CCTCACTCTC TTCCGCATCG  
601 CTGTCTGCGA GGGCCAGCTG TTGGGCTCGC GGTTGAGGAC AAACCTCTTC  
651 CGGTCTTTCC AGTACTCTTG GATCGGAAAC CCGTCGGCCT CCGAACGGTA  
701 CTCCGCCACC GAGGGACCTG AGCGAGTCCG CATCGACCGG ATCGGAAAAC  
751 CTCTCGAGAA AGGCGTCTAA CCAGTCACAG TCGCAAGGTA GGCTGAGCAC  
801 CGTGGCGGGC GGCAGCGGGT GGCGGTCTGG GTTGTTTCTG GCGGAGGTGC  
851 TGCTGATGAT GTAATTAAAG TAGGCGGTCT TGAGACGGCG GATGGTCGAG  
901 GTGAGGTGTG GCAGGCTTGA GATCGATCTG GCCATACACT TGAGTGACAA  
951 TGACATECAC TTTGCCTTTC TCTCCACAGG TGTCCACTCC CAGGTCCAAC  
1001 TGGATCCAAG CTTCGACTCG AGGAATTCCC CGAAGGAACA AAGCACCTC  
1051 CCCACTGGGC TCCTGGTTGC AGAGCTCCAA GTCCTCACAC AGATACGCCT  
1101 GTTTGAGAAG CAGCGGGCAA GAAAGACGCA AGCCAGAGG CCCTGCCATT  
1151 TCTGTGGGCT CAGGTCCCTA CTGGCTCAGG CCCCTGCCTC CCTCGGCAAG  
1201 GCCACAATGA ACCGGGGAGT CCCTTTTAGG CACTTGCTTC TGGTGCTGCA  
1251 ACTGGCGCTC CTCCCAGCAG CCACTCAGGG AAAGAAAGTG GTGCTGGGCA  
1301 AAAAAGGGGA TACAGTGGAA CTGACCTGTA CAGCTTCCCA GAAGAAGAGC  
1351 ATACAATTCC ACTGGAAAAA CTCCAACCAG ATAAAGATTC TGGGAAATCA  
1401 GGGCTCCTTC TTAACCTAAC GTCCATCCAA GCTGAATGAT CCGCTGACT

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*FIG. 15(con't'd)*

1451 CAAGAAGAAG CTTGTGGGAC CAAGGAAACT TTCCCTGAT CATCAAGAAT  
 1501 CTTAAGATAG AAGACTCAGA TACTTACATC TGTGAAGTGG AGGACCAGAA  
 1551 GGAGGAGGTG CAATTGCTAG TGTTCGGATT GACTGCCAAC TCTGACACCC  
 1601 ACCTGCTTCA GGGGCAGAGC CTGACCCTGA CCTTGGAGAG CCCCCCTGGT  
 1651 AGTAGCCCCCT CAGTGCAATG TAGGAGTCCA AGGGGTAAAA ACATACAGGG  
 1701 GGGGAAGACC CTCTCCGTGT CTCAGCTGGA GCTCCAGGAT AGTGGCACCT  
 1751 GGACATGCAC TGTCTTGCAG AACCAGAAGA AGETGGAGTT CAAAATAGAC  
 1801 ATCGTGGTGC TAGCTTTCCA GAAGGCCTCC AGCATAGTCT ATAAGAAAGA  
 1851 GGGGGAACAG GTGGAGTTCT CCTTCCCACT CGCCTTTACA GTTGAAAAGC  
 1901 TGACGGGCAG TGGCGAGCTG TGGTGGCAGG CGGAGAGGGC TTCCTCCTCC  
 1951 AAGTCTTGGA TCACCTTTGA CCTGAAGAAC AAGGAAGTGT CTGTAAAACG  
 2001 GGTTACCCAG GACCCTAAGC TCCAGATGGG CAAGAAGCTC CCGCTCCACC  
 2051 TCACCCTGCC CCAGGCCTTG CCTCAGTATG CTGGCTCTGG AAACCTCACC  
 2101 CTGGCCCTTG AAGCGAAAAC AGGAAAGTTG CATCAGGAAG TGAACCTGGT  
 2151 GGTGATGAGA GCCACTCAGC TCCAGAAAAA TTTGACCTGT GAGGTGTGGG  
 2201 GACCCACCTC CCCTAAGCTG ATGCTGAGTT TGAAACTGGA GAACAAGGAG  
 2251 GCAAAGGTCT CGAAGCGGGA GAAGGCGGTG TGGGTGCTGA ACCCTGAGGC  
 2301 GGGGATGTGG CAGTGTCTGC TGAGTGA CTG GGGACAGGTC CTGCTGGAAT  
 2351 CCAACATCAA GGTTCTGCCC ACATGGTCTGA CCCCAGGTGCA GCCAATGGCC  
 2401 CTGATTTGAG ATCTTTGTGA AGGAACCTTA CTTCTGTGGT GTGACATAAT  
 2451 TGGACAAACT ACCTACAGAG ATTTAAAGCT CTAAGGTAAT TATAAAATTT  
 2501 TTAAGTGTAT AATGTGTTAA ACTACTGATT CTAATTGTTT GTGTATTTTA  
 2551 GATTCCAACC TATGGAAGCTG ATGAATGGGA GCAGTGGTGG AATGCCTTTA  
 2601 ATGAGGAAAA CCTGTTTTGC TCAGAAGAAA TGCCATCTAG TGATGATGAG  
 2651 GCTACTGCTG ACTCTCAACA TTCTACTCCT CCAAAAAAGA AGAGAAAGGT  
 2701 AGAAGACCCC AAGGACTTTC CTTCAGAATT GCTAAGTTTT TTGAGTCATG  
 2751 CTGTGTTTAG TAATAGAACT CTTGCTTGCT TTGCTATTTA CACCACAAAG  
 2801 GAAAAAGCTG CACTGCTATA CAAGAAAATT ATGGAAAAAT ATTCTGTAAC  
 2851 CTTTATAAGT AGGCATAACA GTTATAATCA TAACATACTG TTTTTCTTA  
 2901 CTCCACACAG GCATAGAGTG TCTGCTATTA ATAACATATGC TCAAAAATTG  
 2951 TGTACCTTTA GCTTTTTAAT TTGTAAAGGG GTTAATAAGG AATATTTGAT  
 3001 GTATAGTGCC TTGACTAGAG ATCATAATCA GCCATACCAC ATTTGTAGAG  
 3051 GTTTTACTTG CTTTAAATTAATCTGCAACAC CTCCCCTGA ACCTGAAACA

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*F1G.15(cont'd)*

3101 TAAATGAAT GCAATTGTTG TTGTTAALIT GTTTATTGCA GCTTATAATG  
 3151 GTTACAAATA AAGCAATAGC ATCACAAATT TCACAAATAA AGCATTTTTT  
 3201 TCACTGCATT CTAGTTGTGG TTTGTCCAAA CTCATCAATG TATCTTATCA  
 3251 TGTCTGGATC CTCTACGCCG GACGCATCGT GGCCGGCATC ACCGGCGCCA  
 3301 CAGGTGCGGT TGCTGGCGCC TATATCGCCG ACATCACCGA TGGGGAAGAT  
 3351 CGGGCTCGCC ACTTCGGGCT CATGAGCGCT TGTTTCGGCG TGGGTATGGT  
 3401 GGCAGGCCCC TGGCCGGGGG ACTGTTGGGC GCCATCTCCT TGCATGCACC  
 3451 ATTCCTTGCG GCGGCGGTGC TCAACGGCCT CAACCTACTA CTGGGCTGCT  
 3501 TCCTAATGCA GGAGTCGCAT AAGGGAGAGC GTCGACCGAT GCCCTTGAGA  
 3551 GCCTTCAACC CAGTCAGCTC CTTCCGGTGG GCGCGGGGCA TGA CTATCGT  
 3601 CGCCGCACTT ATGACTGTCT TCTTTATCAT GCAACTCGTA GGACAGGTGC  
 3651 CGGCAGCGCT CTGGGTCATT TTCGGCGAGG ACCGCTTTCG CTGGAGCGCG  
 3701 ACGATGATCG GCCTGTGCTG TCGGGTATTC GGAATCTTGC ACGCCCTCGC  
 3751 TCAAGCCTTC GTCACTGGTC CCGCCACCAA ACGTTTCGGC GAGAAGCAGG  
 3801 CCATTATCGC CGGCATGGCG GCCGACGCGC TGGGCTACGT CTTGCTGGCG  
 3851 TTCGCGACGC GAGGCTGGAT GGCCTTCCCC ATTATGATTC TTCTCGCTTC  
 3901 CGGCGGCATC GGGATGCCCG CGTTGCAGGC CATGCTGTCC AGGCAGGTAG  
 3951 ATGACGACCA TCAGGGACAG CTTCAAGGAT CGCTCGCGGC TCTTACCAGC  
 4001 CTA ACTTCGA TCACTGGACC GCTGATCGTC ACGGCGATTT ATGCCGCCTC  
 4051 GGCGAGCACA TGGAACGGGT TGGCATGGAT TGTAGGCGCC GCCCTATACC  
 4101 TTGTCTGCCT CCCC GCGTTG CGTCGCGGTG CATGGAGCCG GGCCACCTCG  
 4151 ACCTGAATGG AAGCCGGCGG CACCTCGCTA ACGGATTAC CACTCCAAGA  
 4201 ATTGGAGCCA ATCAATTCTT GCGGAGAACT GTGAATGCGC AAACCAACCC  
 4251 TTGGCAGAAC ATATCCATCG CGTCCGCCAT CTCCAGCAGC CGCACGCGGC  
 4301 GCATCTCGGG CCGCGTTGCT GCGGTTTTTC CATAGGCTCC GCCCCCTGA  
 4351 CGAGCATCAC AAAAATCGAC GCTCAAGTCA GAGGTGGCGA AACCCGACAG  
 4401 GACTATAAAG ATACCAGGCG TTTCCCCCTG GAAGCTCCCT CGTGCGCTCT  
 4451 CCTGTTCCGA CCCTGCCGCT TACCGGATAC CTGTCCGCCT TTCTCCCTTC  
 4501 GGGAAAGCGTG GCGCTTTCTC AATGCTCAGC CTGTAGGTAT CTCAGTTCGG  
 4551 TGTAGGTCGT TCGCTCCAAG CTGGGCTGTG TGCACGAACC CCCC GTTCAG  
 4601 CCCGACCGCT GCGCCTTATC CGGTA ACTAT CGTCTTGAGT CCAACCCGGT  
 4651 AAGACACGAC TTATCGCCAC TGGCAGCAGC CACTGGTAAC AGGATTAGCA  
 4701 GAGCGAGGTA TGTAAGCGAT GCTACAGAGT TCTTGAAGTG GTGGCCTAAC

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*FIG. 15(cont'd)*

4751 TACGGCTACA CTAGAAGGAC AGTATTTGGT ATCTGCGCTC TGCTGAAGCC  
4801 AGTTACCTTC GGAAAAAGAG TTGGTAGCTC TTGATCCGGC AAACAAACCA  
4851 CCGCTGGTAG CGGTGGTTTT TTTGTTTGCA AGCAGCAGAT TACGCGCAGA  
4901 AAAAAAGGAT CTCAAGAAGA TCCTTTGATC TTTTCTACGG GGTCTGACGC  
4951 TCAGTGGAAC GAAAACTCAC GTTAAGGGAT TTTGGTCATG AGATTATCAA  
5001 AAAGGATCTT CACCTAGATC CTTTTAAATT AAAAATGAAG TTTTAAATCA  
5051 ATCTAAAGTA TATATGAGTA AACTTGGTCT GACAGTTACC AATGCTTAAT  
5101 CAGTGAGGCA CCTATCTCAG CGATCTGTCT ATTTCGTTCA TCCATAGTTG  
5151 CCTGACTCCC CGTCGTGTAG ATAACACGA TACGGGAGGG CTTACCATCT  
5201 GGCCCCAGTG CTGCAATGAT ACCGCGAGAC CCACGCTCAC CGGCTCCAGA  
5251 TTTATCAGCA ATAAACCAGC CAGCCGGAAG GGCCGAGCGC AGAAGTGGTC  
5301 CTGCAACTTT ATCCGCCTCC ATCCAGTCTA TTAATTGTTG CCGGGAAGCT  
5351 AGAGTAAGTA GTTCGCCAGT TAATAGTTTG CGCAACGTTG TTGCCATTGC  
5401 TGCAGGCATC GTGGTGTAC GCTCGTCGTT TGGTATGGCT TCATTACAGT  
5451 CCGGTTCCCA ACGATCAAGG CGAGTTACAT GATCCCCCAT GTTGTGCAAA  
5501 AAAGCGGTTA GCTCCTTCGG TCCTCCGATC GTTGTGAGAA GTAAGTTGGC  
5551 CGCAGTGTTA TCACTCATGG TTATGGCAGC ACTGCATAAT TCTCTTACTG  
5601 TCATGCCATC CGTAAGATGC TTTTCTGTGA CTGGTGAGTA CTCAACCAAG  
5651 TCATTCTGAG AATAGTGTAT GCGGCGACCG AGTTGCTCTT GCGCGGCGTC  
5701 AACACGGGAT AATACCGCGC CACATAGCAG AACTTTAAAA GTGCTCATCA  
5751 TTGGAAAACG TTCTTCGGGG CGAAAACTCT CAAGGATCTT ACCGCTGTTG  
5801 AGATCCAGTT CGATGTAACC CACTCGTGCA CCCAACTGAT CTTCAGCATC  
5851 TTTTACTTTC ACCAGCGTTT CTGGGTGAGC AAAAACAGGA AGGCAAAATG  
5901 CCGCAAAAAA GGAATAAGG GCGACACGGA AATGTTGAAT ACTCATACTC  
5951 TTCCTTTTTT AATATTATTG AAGCATTTAT CAGGGTTATT GTCTCATGAG  
6001 CGGATACATA TTTGAATGTA TTTAGAAAAA TAAACAAATA GGGGTTCCGC  
6051 GCACATTTCC CCGAAAAGTG CCACCTGACG TCTAAGAAAC CATTATTATC  
6101 ATGACATTAA CCTATAAAAA TAGGCGTATC ACGAGGCCCT TTCGTCTTCA  
6151 A

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p86392  
 :86368 backbone  
 :soluble T4#7  
 :AA #3 = LVS  
 :182AA+6AA  
 :from 203-5

FIG. 16

bp392.seq Length: 6149

1 GAATTAATTC CAGCTTGCTG TGAATGTGT GTCAGTTAGG GTGTGGAAAG  
 51 TCCCCAGGCT CCCCAGCAGG CAGAAGTATG CAAAGCATGC ATCTCAATTA  
 101 GTCAGCAACC AGGTGTGGAA AGTCCCCAGG CTCCCCAGCA GGCAGAAGTA  
 151 TGCAAAGCAT GCATCTCAAT TAGTCAGCAA CCATAGTCCC GCCCCTAACT  
 201 CCGCCCATCC CGCCCCTAAC TCCGCCCAGT TCCGCCCATT CTCCGCCCCA  
 251 TGGCTGACTA ATTTTTTTTA TTTATGCAGA GGCCGAGGCC GCCTCGGCCT  
 301 CTGAGCTATT CCAGAAGTAG TGAGGAGGCT TTTTGGAGG GGTCTCTCTC  
 351 GTATAGAAAC TCGGACCACT CTGAGACGAA GGCTCGCGTC CAGGCCAGCA  
 401 CGAAGGAGGC TAAGTGGGAG GGGTAGCGGT CGTTGTCCAC TAGGGGGTCC  
 451 ACTCGCTCCA GGGTGTGAAG ACACATGTCG CCCTCTTCGG CATCAAGGAA  
 501 GGTGATTGGT TTATAGGTGT AGGCCACGTG ACCGGGTGTT CCTGAAGGGG  
 551 GGCTATAAAA GGGGGTGGGG GCGCGTTCGT CCTCACTCTC TTCCGCATCG  
 601 CTGTCTGCGA GGGCCAGCTG TTGGGCTCGC GGTGAGGAC AAACCTCTTCG  
 651 CGGTCTTTCC AGTACTCTTG GATCGGAAAC CCGTCGGCCT CCGAACGGTA  
 701 CTCCGCCACC GAGGGACCTG AGCGAGTCCG CATCGACCGG ATCGGAAAAC  
 751 CTCTCGAGAA AGGCGTCTAA CCAGTCACAG TCGCAAGGTA GGCTGAGCAC  
 801 CGTGGCGGGC GGCAGCGGGT GGCGGTCGGG GTTGTCTCTG GCGGAGGTGC  
 851 TGCTGATGAT GTAATTAAG TAGGCGGTCT TGAGACGGCG GATGGTCGAG  
 901 GTGAGGTGTG GCAGGCTTGA GATCGATCTG GCCATACACT TGAGTGACAA  
 951 TGACATCCAC TTTGCCTTC TCTCCACAGG TGTCCACTCC CAGGTCCAAC  
 1001 TGGATCCAAG CTTCGACTCG AGGAATTCCC CGAAGGAACA AAGCACCCCT  
 1051 CCCACTGGGC TCCTGGTTGC AGAGCTCAA GTCCTCACAC AGATACGCCT  
 1101 GTTTGAGAAG CAGCGGGCAA GAAAGACGCA AGCCAGAGG CCCTGCCATT  
 1151 TCTGTGGGCT CAGGTCCCTA CTGGCTCAGG CCCCTGCCTC CCTCGGCAAG  
 1201 GCCACA<sup>MET</sup>ATGA ACCGGGGAGT CCCTTTTAGG CACTTGCTTC TGGTGCTGCA  
 1251 ACTGGCGCTC CTCCCAGCAG CCACTCAGGG<sup>AA-23</sup> AAAGAAAGTG GTGCTGGGCA  
 1301 AAAAAAGGGA TACAGTGGAA<sup>AA1</sup>CTGACCTTA CAGCTTCCCA GAAGAAGAGC  
 1351 ATACAATTCC ACTGGAAAAA CTCCAACCAG ATAAAGATTG TGGGAAATCA

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FIG. 16(cont'd)

1401 GGGCTCCTTC TTAACATAAG GTCCATCCAA GCTGAATGAT CGCGCTGACT  
 1451 CAAGAAGAAG CTTGTGGGAC CAAGGAACT TTCCCCTGAT CATCAAGAAT  
 1501 CTTAAGATAG AAGACTCAGA TACTTACATC TGTGAAGTGG AGGACCAGAA  
 1551 GGAGGAGGTG CAATTGCTAG TGTTCGGATT GACTGCCAAC TCTGACACCC  
 1601 ACCTGCTTCA GGGGCAGAGC CTGACCCTGA CCTTGGAGAG CCCCCCTGGT  
 1651 AGTAGCCCCCT CAGTGCAATG TAGGAGTCCA AGGGGTAAAA ACATACAGGG  
 1701 GGGGAAGACC CTCTCCGTGT CTCAGCTGGA GCTCCAGGAT AGTGGCACCT  
 1751 GGACATGCAC TGTCTTGCA G AACCAGAAGA AGGTGGAGTT CAAAATAGAC  
 1801 ATCGTGGTGC TAGCTTTCCA GAACCTCCAG CATAGTCTAT <sup>STOP</sup> AAGAAAGAGG  
 1851 GGGAACAGGT GGAGTTCTCC TTCCCCTCG CCTTTACAGT TGAAAAGCTG  
 1901 ACGGGCAGTG GCGAGCTGTG GTGGCAGGCG GAGAGGGCTT CCTCCTCCAA  
 1951 GTCTTGATC ACCTTTGACC TGAAGAACAA GGAAGTGTCT GTAAAACGGG  
 2001 TTACCCAGGA CCCTAAGCTC CAGATGGGCA AGAAGCTCCC GCTCCACCTC  
 2051 ACCCTGCCCC AGGCCTTGCC TCAGTATGCT GGCTCTGGAA ACCTCACCT  
 2101 GGCCCTTGAA GCGAAAACAG GAAAGTTGCA TCAGGAAGTG AACCTGGTGG  
 2151 TGATGAGAGC CACTCAGCTC CAGAAAAATT TGACCTGTGA GGTGTGGGGA  
 2201 CCCACCTCCC CTAAGCTGAT GCTGAGTTTG AACTGGAGA ACAAGGAGGC  
 2251 AAAGGTCTCG AAGCGGGAGA AGGCGGTGTG GGTGCTGAAC CCTGAGGCGG  
 2301 GGATGTGGCA GTGTCTGCTG AGTGAATCGG GACAGGTCCT GCTGGAATCC  
 2351 AACATCAAGG TTCTGCCCAC ATGGTGCACC CCGGTGCAGC CAATGGCCCT  
 2401 GATTTGAGAT CTTTGTGAAG GAACCTTACT TCTGTGGTGT GACATAATTG  
 2451 GACAACTAC CTACAGAGAT TAAAGCTCT AAGGTAAATA TAAATTTTT  
 2501 AAGTGATAA TGTGTTAAAC TACTGATTCT AATTGTTTGT GTATTTTAGA  
 2551 TTCCAACCTA TGGAAGTAT GAATGGGAGC AGTGGTGGAA TGCCTTTAAT  
 2601 GAGGAAAACC TGTTTTGCTC AGAAGAAATG CCATCTAGTG ATGATGAGGC  
 2651 TACTGCTGAC TCTCAACATT CTAATCCTCC AAAAAAGAAG AGAAAGGTAG  
 2701 AAGACCCCAA GGACTTTCTC TCAGAATTGC TAAGTTTTTT GAGTCATGCT  
 2751 GTGTTTAGTA ATAGAACTCT TGCTTGCTTT GCTATTTACA CCACAAAGGA  
 2801 AAAAGCTGCA CTGCTATACA AGAAAATTAT GGAAAAATAT TCTGTAACCT  
 2851 TTATAAGTAG GCATAACAGT TATAATCATA ACATACTGTT TTTTCTTACT  
 2901 CCACACAGGC ATAGAGTGTC TGCTATTAAT AACTATGCTC AAAAATTGTG  
 2951 TACCTTTAGC TTTTAAATT GTAAAGGGGT TAATAAGGAA TATTTGATGT  
 3001 ATAGTGCCCT GACTAGAGAT CATAATCAGC CATACCACAT TTGTAGAGGT

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*FIG. 16(cont'd)*

3051 TTTACTTGCT TTAAAAAAC TCCACAC T CCCCCTGAAC CTGAAACATA  
3101 AAATGAATGC AATTGTTGTT GTTAACTTGT TTATTGCAGC TTATAATGGT  
3151 TACAAATAAA GCAATAGCAT CACAAATTTT CAAAATAAAG CATTTTTTTT  
3201 ACTGCATTCT AGTTGTGGTT TGTCCAACT CATCAATGTA TCTTATCATG  
3251 TCTGGATCCT CTACGCCGGA CGCATCGTGG CCGGCATCAC CGGCGCCACA  
3301 GGTGCGGTTG CTGGCGCCTA TATCGCCGAC ATCACCGATG GGGAAGATCG  
3351 GGCTCGCCAC TTCGGGCTCA TGAGCGCTTG TTTCGGCGTG GGTATGGTGG  
3401 CAGGCCCGTG GCCGGGGGAC TGTTGGGCGC CATCTCCTTG CATGCACCAT  
3451 TCCTTGCGGC GGCGGTGCTC AACGGCCTCA ACCTACTACT GGGCTGCTTC  
3501 CTAATGCAGG AGTCGCATAA GGGAGAGCGT CGACCGATGC CCTTGAGAGC  
3551 CTTCAACCCA GTCAGCTCCT TCCGGTGGGC GCGGGGCATG ACTATCGTCG  
3601 CCGCACTTAT GACTGTCTTC TTTATCATGC AACTCGTAGG ACAGGTGCCG  
3651 GCAGCGCTCT GGGTCATTTT CGGCGAGGAC CGCTTTCGCT GGAGCGCGAC  
3701 GATGATCGGC CTGTGCTTG CGGTATTCGG AATCTTGAC GCCCTCGCTC  
3751 AAGCCTTCGT CACTGGTCCC GCCACCAAAC GTTTCGGCGA GAAGCAGGCC  
3801 ATTATCGCCG GCATGGCGGC CGACGCGCTG GGCTACGTCT TGCTGGCGTT  
3851 CGCGACGCGA GGCTGGATGG CCTTCCCCAT TATGATTCTT CTCGCTTCCG  
3901 GCGGCATCGG GATGCCCGCG TTGCAGGCCA TGCTGTCCAG GCAGGTAGAT  
3951 GACGACCATC AGGGACAGCT TCAAGGATCG CTCGCGGCTC TTACCAGCCT  
4001 AACTTCGATC ACTGGACCGC TGATCGTCAC GGCGATTTAT GCCGCTCGG  
4051 CGAGCACATG GAACGGGTTG GCATGGATTG TAGGCGCCGC CCTATACCTT  
4101 GTCTGCCTCC CCGCGTTGCG TCGCGGTGCA TGGAGCCGGG CCACCTCGAC  
4151 CTGAATGGAA GCCGGCGGCA CCTCGCTAAC GGATTCACCA CTCCAAGAAT  
4201 TGGAGCCAAT CAATTCTTGC GGAGAACTGT GAATGCGCAA ACCAACCCTT  
4251 GGCAGAACAT ATCCATCGCG TCCGCCATCT CCAGCAGCCG CACGCGGCGC  
4301 ATCTCGGGCC GCGTTGCTGG CGTTTTTCCA TAGGCTCCGC CCCCCTGACG  
4351 AGCATCACAA AAATCGACGC TCAAGTCAGA GGTGGCGAAA CCCGACAGGA  
4401 CTATAAAGAT ACCAGGCGTT TCCCCCTGGA AGCTCCCTCG TCGCTCTCC  
4451 TGTTCGACC CTGCCGCTTA CCGGATACCT GTCCGCCTTT CTCCCTTCGG  
4501 GAAGCGTGGC GCTTCTCAA TGCTCACGCT GTAGGTATCT CAGTTCGGTG  
4551 TAGGTCGTTT GCTCCAAGCT GGGCTGTGTG CACGAACCCC CCGTTCAGCC  
4601 CGACCGCTGC GCCTTATCCG GTAACATCG TCTTGAGTCC AACCCGGTAA  
4651 GACACGACTT ATCGCCACTG GCAGCAGCCA CTGGTAACAG GATTAGCAGA

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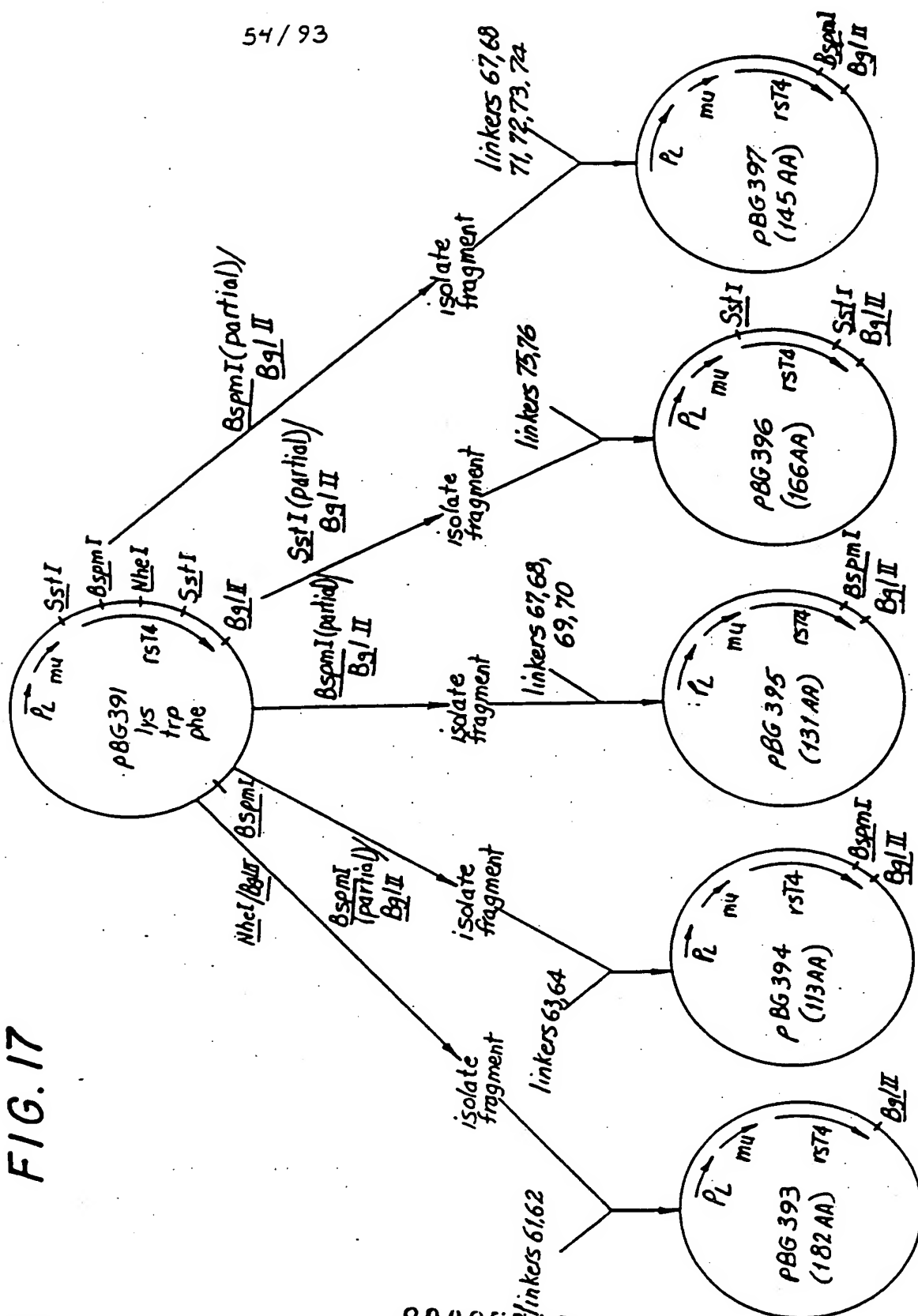
*FIG. 16(cont'd)*

4701 GCGAGGTATG TAGGCGGTGC TACAGAGTTC TTGAAGTGGT GGCCTAACTA  
4751 CGGCTACACT AGAAGGACAG TATTTGGTAT CTGCGCTCTG CTGAAGCCAG  
4801 TTACCTTCGG AAAAAGAGTT GCTAGCTCTT GATCCGGCAA ACAAACCACC  
4851 GCTGGTAGCG GTGGTTTTTT TGTTCGCAAG CAGCAGATTA CGCGCAGAAA  
4901 AAAAGGATCT CAAGAAGATC CTTTGATCTT TTCTACGGGG TCTGACGCTC  
4951 AGTGGAACGA AAACACAGT TAAGGGATTT TGGTCATGAG ATTATCAAAA  
5001 AGGATCTTCA CCTAGATCCT TTAAATTA AAATGAAGTT TAAATCAAT  
5051 CTAAAGTATA TATGAGTAAA CTTGGTCTGA CAGTTACCAA TGCTTAATCA  
5101 GTGAGGCACC TATCTCAGCG ATCTGTCTAT TTCGTTTCATC CATAGTTGCC  
5151 TGAATCCCCG TCGTGTAGAT AACTACGATA CGGGAGGGCT TACCATCTGG  
5201 CCCCAGTGCT GCAATGATAC CGCGAGACCC ACGCTCACCG GCTCCAGATT  
5251 TATCAGCAAT AAACCAGCCA GCCGGAAGGG CCGAGCGCAG AAGTGGTCCT  
5301 GCAACTTTAT CCGCTCCAT CCAGTCTATT AATTGTTGCC GGAAGCTAG  
5351 AGTAAGTAGT TCGCCAGTTA ATAGTTTGGC CAACGTTGTT GCCATTGCTG  
5401 CAGGCATCGT GGTGTCACGC TCGTCGTTTG GTATGGCTTC ATTCAGCTCC  
5451 GGTTCCCAAC GATCAAGGCG AGTTACATGA TCCCCCATGT TGTGCAAAAA  
5501 AGCGGTTAGC TCCTTCGGTC CTCCGATCGT TGTGAGAAGT AAGTTGGCCG  
5551 CAGTGTTATC ACTCATGGTT ATGGCAGCAC TGCATAATTC TCTTACTGTC  
5601 ATGCCATCCG TAAGATGCTT TTCTGTGACT GGTGAGTACT CAACCAAGTC  
5651 ATTCTGAGAA TAGTGTATGC GGCGACCGAG TTGCTCTTGC CCGGCGTCAA  
5701 CACGGGATAA TACCGCGCCA CATAGCAGAA CTTTAAAAGT GCTCATCATT  
5751 GGAAAACGTT CTTCGGGGCG AAAACTCTCA AGGATCTTAC CGCTGTTGAG  
5801 ATCCAGTTCG ATGTAACCCA CTCGTGCACC CAACTGATCT TCAGCATCTT  
5851 TTACTTTTAC CAGCGTTTCT GGGTGAGCAA AAACAGGAAG GCAAAATGCC  
5901 GCAAAAAAGG GAATAAGGGC GACACGGAAA TGTGAATAC TCATACTCTT  
5951 CCTTTTTCAA TATTATTGAA GCATTTATCA GGGTTATTGT CTCATGAGCG  
6001 GATACATATT TGAATGTATT TAGAAAAATA AACAAATAGG GGTTCCGCGC  
6051 ACATTTCCCC GAAAAGTCCC ACCTGACGTC TAAGAAACCA TTATTATCAT  
6101 GACATTAACC TATAAAAATA GGCGATCAC GAGGCCCTTT CGTCTTCAA

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FIG. 17



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FIG. 18

61 5' CTA CCT TTT CCA GTG A 3'

62 5' GAT CTC ACT CGA AAG 3'

63 5' CCG GTG ATA GTA A 3'

64 5' GAT CTT ACT ATC A 3'

67 5' CCG CCA GAG CCT GAC CCT GAC CTT CGA GAG CCC C 3'

68 5' CCG CCG GGC TGT CCA AGG TCA CCG TCA GGC TGT G 3'

69 5' CCG CCG AGT AGC CCC TCA GTG CAA TCA 3'

70 5' GAT CTC ATT CCA CTC AGG GGC TAC TAC 3'

71 5' CCG CCG AGT AGC CCC TCA GTG CAA TGT AGG AGT C 3'

72 5' TAG GAC TCC TAC ATT CCA CTC AGG GGC TAC TAC 3'

73 5' CTA CCG GTA AAA ACA TAC AGG CCG CGA AGA CCT GA 3'

74 5' GAT CTC AGG TGT TTC CCC CCC TGT ATG TTT TTA CCC 3'

75 5' CCA CGA TAG TCG CAC CTC GAC ATG CAC TGT CTT GCA  
GAA CTC A 3'

76 5' GAT CTC AGT TGT CCA AGA CAG TCG ATG TCG AGG TCG  
CAC TAT CCT CGA CTT 3'

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pBG394  
 :BG368 backbone  
 :soluble T4#9  
 :AA #3 = LVS  
 :first 113 AA of T4  
 :basically up to VIJ1

FIG. 19

bg394.seq Length: 5365

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1  GAATTAATTC CAGCTTGCTG TGAATGTGT GTCAGTTAGG GTGTGGAAAG
51  TCCCCAGGCT CCCCAGCAGG CAGAAGTATG CAAAGCATGC ATCTCAATTA
101 GTCAGCAACC AGGTGTGGAA AGTCCCCAGG CTCCCCAGCA GGCAGAAGTA
151 TGCAAAGCAT GCATCTCAAT TAGTCAGCAA CCATAGTCCC GCCCCTAACT
201 CCGCCCATCC CGCCCCTAAC TCCGCCCAGT TCCGCCCATC CTCCGCCCCA
251 TGGCTGACTA ATTTTTTTTA TTTATGCAGA GGCCGAGGCC GCCTCGGCCT
301 CTGAGCTATT CCAGAAGTAG TGAGGAGGCT TTTTGGAGG GGTCTCTCTC
351 GTATAGAAAC TCGGACCACT CTGAGACGAA GGCTCGCGTC CAGGCCAGCA
401 CGAAGGAGGC TAAGTGGGAG GGGTAGCGGT CGTTGTCCAC TAGGGGGTCC
451 ACTCGCTCCA GGGTGTGAAG ACACATGTCT CCCTCTTCGG CATCAAGGAA
501 GGTGATTGGT TTATAGGTGT AGGCCACGTG ACCGGGTGTT CCTGAAGGGG
551 GGCTATAAAA GGGGGTGGGG GCGCGTTCGT CCTCACTCTC TTCCGCATCG
601 CTGTCTGCGA GGGCCAGCTG TTGGGCTCGC GGTTGAGGAC AAACTCTTCG
651 CGGTCTTTCC AGTACTCTTG GATCGGAAAC CCGTCGGCCT CCGAACGGTA
701 CTCCGCCACC GAGGGACCTG AGCGAGTCCG CATCGACCGG ATCGGAAAAC
751 CTCTCGAGAA AGGCGTCTAA CCAGTCACAG TCGCAAGGTA GGCTGAGCAC
801 CGTGGCGGGC GGCAGCGGGT GGCGGTCTGG GTTGTCTCTG GCGGAGGTGC
851 TGCTGATGAT GTAATTAAG TAGGCGGTCT TGAGACGGCG GATGGTCGAG
901 GTGAGGTGTG GCAGGCTTGA GATCGATCTG GCCATACACT TGAGTGACAA
951 TGACATCCAC TTGCTCTTC TCTCCACAGG TGTCCTCTCC CAGGTCCAAC
1001 TGGATCCAAG CTTCGACTCG AGGAATTCCC CGAAGGAACA AAGCACCTC
1051 CCCACTGGGC TCCTGGTTGC AGAGCTCCAA GTCCTCACAC AGATACGCCT
1101 GTTGTGAGAAG CAGCGGGCAA GAAAGACGCA AGCCCAGAGG CCCTGCCATT
1151 TCTGTGGGCT CAGGTCCCTA CTGGCTCAGG CCCCTGCCTC CCTCGGCAAG
1201 GCCACAATGA ACCGGGGAGT CCCTTTTAGG CACTTGCTTC TGGTGCTGCA
1251 ACTGGCGCTC CTCCCAGCAG CCACTCAGGG AAAGAAAGTG GTGCTGGGCA
1301 AAAAAGGGGA TACAGTGGAA CTGACCTGTA CAGCTTCCCA GAAGAAGAGC
1351 ATACAAATTC ACTGACCTGCA ACCAG ATAAAGATTC TGGGAAATCA

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## F!G.19 (cont'd)

1401 GGGCTCCTTC TTAACATAAG GTCCATCCAA GCTGAATGAT CGCGCTGACT  
 1451 CAAGAAGAAG CTTGTGGGAC CAAGGAAACT TTCCCTGAT CATCAAGAAT  
 1501 CTTAAGATAG AAGACTCAGA TACTTACATC TGTGAAGTGG AGGACCAGAA  
 1551 GGAGGAGGTG CAATTGCTAG TGTTCGGATT GACTGCCAAC TCTGACACCC  
 1601 ACCTGCTTCA GGGGTGATAG TAAGATCTTT GTGAAGGAAC CTTACTTCTG  
 1651 TGGTGTGACA TAATTGGACA AACTACCTAC AGAGATTTAA AGCTCTAAGG  
 1701 TAAATATAAA ATTTTAAAGT GTATAATGTG TTAAACTACT GATTCTAATT  
 1751 GTTGTGTAT TTTAGATTCC AACCTATGGA ACTGATGAAT GGGAGCAGTG  
 1801 GTGGAATGCC TTTAATGAGG AAAACCTGTT TTGCTCAGAA GAAATGCCAT  
 1851 CTAGTGATGA TGAGGCTACT GCTGACTCTC AACATTCTAC TCCTCCAAAA  
 1901 AAGAAGAGAA AGGTAGAAGA CCCCAAGGAC TTTCCTTCAG AATTGCTAAG  
 1951 TTTTTTGAGT CATGCTGTGT TTAGTAATAG AACTCTTGCT TGCTTTGCTA  
 2001 TTTACACCAC AAAGGAAAAA GCTGCACTGC TATACAAGAA AATTATGGAA  
 2051 AAATATTCTG TAACCTTTAT AAGTAGGCAT AACAGTTATA ATCATAACAT  
 2101 ACTGTTTTTT CTTACTCCAC ACAGGCATAG AGTGTCTGCT ATTAATAACT  
 2151 ATGCTCAAAA ATTGTGTACC TTTAGCTTTT TAATTTGTAA AGGGGTTAAT  
 2201 AAGGAATATT TGATGTATAG TGCCTTGACT AGAGATCATA ATCAGCCATA  
 2251 CCACATTTGT AGAGGTTTTA CTTGCTTTAA AAAACCTCCC ACACCTCCCC  
 2301 CTGAACCTGA AACATAAAAT GAATGCAATT GTTGTGTGTA ACTTGTTTTAT  
 2351 TGCAGCTTAT AATGGTTACA AATAAAGCAA TAGCATCACA AATTTACAAA  
 2401 ATAAAGCATT TTTTCACTG CATTCTAGTT GTGGTTTGTC CAAACTCATC  
 2451 AATGTATCTT ATCATGTCTG GATCCTCTAC GCCGGACGCA TCGTGGCCGG  
 2501 CATCACCGGC GCCACAGGTG CGGTTGCTGG CGCCTATATC GCCGACATCA  
 2551 CCGATGGGGA AGATCGGGCT CGCCACTTCG GGCTCATGAG CGCTTGTTTC  
 2601 GCGGTGGGTA TGGTGGCAGG CCGGTGGCCG GGGGACTGTT GGGCGCCATC  
 2651 TCCTTGCAATG CACCATTCCT TCGCGCGGCG GTGCTCAACG GCCTCAACCT  
 2701 ACTACTGGGC TGCTTCCTAA TGCAGGAGTC GCATAAGGGA GAGCGTCGAC  
 2751 CGATGCCCTT GAGAGCCTTC AACCCAGTCA GCTCCTTCGG GTGGGCGCGG  
 2801 GGCATGACTA TCGTCGCCGC ACTTATGACT GTCTTCTTTA TCATGCAACT  
 2851 CGTAGGACAG GTGCCGGCAG CGCTCTGGGT CATTTTCGGC GAGGACCGCT  
 2901 TTCGCTGGAG CGCGACGATG ATCGGCCTGT CGCTTGCGGT ATTCGGAATC  
 2951 TTGCACGCCC TCGCTCAAGC CTTCGTCAT GGTCCCGCCA CCAAACGTTT  
 3001 CGGCGAGAAG CAGGCCATTA TCGCCGCGAT GCGGCGCGAC GCGCTGGGCT

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# FIG. 19 (cont'd)

305: ACGTCTTGCT GCGGTTCCG GCGGAGGCT GGATGGCCTT CCCATTATG  
 310: ATTCTTCTCG CTTCCGGCGG CATCGGGATG CCJGCGTTGC AGGCCATGCT  
 315: GTCCAGGCAG GTAGATGACG ACCATCAGGG ACAGCTTCAA GGATCGCTCG  
 320: CGGCTCTTAC CAGCCTAACT TCGATCACTG GACCGCTGAT CGTCACGGCG  
 325: ATTTATGCCG CCTCGGCGAG CACATGGAAC GGGTTGGCAT GGATTGTAGG  
 330: CGCCGCCCTA TACCTTGTCT GCCTCCCCGC GTTGCGTCCG GGTGCATGGA  
 335: GCCGGGCCAC CTCGACCTGA ATGGAAGCCG GCGGCACCTC GCTAACGGAT  
 340: TCACCACTCC AAGAATTGGA GCCAATCAAT TCTTGCGGAG AACTGTGAAT  
 345: GCGCAAACCA ACCCTTGGCA GAACATATCC ATCGCGTCCG CCATCTCCAG  
 350: CAGCCGCACG CGGCGCATCT CGGGCCGCGT TGCTGGCGTT TTTCATAGG  
 355: CTCGCCCCC CTGACGAGCA TCACAAAAT CGACGCTCAA GTCAGAGGTG  
 360: GCGAAACCCG ACAGGACTAT AAAGATACCA GCGGTTTCCC CCTGGAAGCT  
 365: CCCTCGTGCG CTCTCCTGTT CCGACCCTGC CGCTTACCGG ATACCTGTCC  
 370: GCCTTTCTCC CTTCCGGAAG CGTGGCGCTT TCTCAATGCT CACGCTGTAG  
 375: GTATCTCAGT TCGGTGTAGG TCGTTCGCTC CAAGCTGGGC TGTGTGCACG  
 380: AACCCCCCGT TCAGCCCGAC CGCTGCGCCT TATCCGGTAA CTATCGTCTT  
 385: GAGTCCAACC CGGTAAGACA CGACTTATCG CCACTGGCAG CAGCCACTGG  
 390: TAACAGGATT AGCAGAGCGA GGTATGTAGG CGGTGCTACA GAGTTCTTGA  
 395: AGTGGTGGCC TAACTACGGC TACACTAGAA GGACAGTATT TGGTATCTGC  
 400: GCTCTGCTGA AGCCAGTTAC CTTCCGAAAA AGAGTTGGTA GCTCTTGATC  
 405: CCGCAAACAA ACCACCGCTG GTAGCGGTGG TTTTTTTGTT TGCAAGCAGC  
 410: AGATTACGCG CAGAAAAAAA GGATCTCAAG AAGATCCTTT GATCTTTTCT  
 415: ACCGGGTCTG ACGCTCAGTG GAACGAAAAC TCACGTTAAG GGATTTTGGT  
 420: CATGAGATTA TCAAAAAGGA TCTTCACCTA GATCCTTTTA AATTAAAAAT  
 425: GAAGTTTTAA ATCAATCTAA AGTATATATG AGTAACTTG GTCTGACAGT  
 430: TACCAATGCT TAATCAGTCA GGCACCTATC TCAGCGATCT GTCTATTTCG  
 435: TTCATCCATA GTTGCTGAC TCCCCGTCGT GTAGATAACT ACGATACGGG  
 440: AGGGCTTACC ATCTGGCCCC AGTGCTGCAA TGATACCGCG AGACCCACGC  
 445: TCACCGGCTC CAGATTTATC AGCAATAAAC CAGCCAGCCG GAAGGGCCGA  
 450: GCGCAGAAGT GGTCTGCAA CTTTATCCGC CTCCATCCAG TCTATTAATT  
 455: GTTGCCGGGA AGCTAGAGTA AGTAGTTCGC CAGTTAATAG TTTGCGCAAC  
 460: GTTGTGCCA TTGCTGCGG CATCGTGGTG TCACGCTCGT CGTTTGGTAT  
 465: GCTTTCATTC AGTCCCGTT CCCAACGATC AAGGCGAGTT ACATGATCCC

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*FIG. 19 (cont'd)*

4701 CCATGTTGTG CAAAAAAGCG GTTAGCTCCT TCGGTCCTCC GATCGTTGTC  
4751 AGAAGTAAGT TGGCCGCAGT GTTATCACTC ATGGTTATGG CAGCACTGCA  
4801 TAATTCTCTT ACTGTCATGC CATCCGTAAG ATGCTTTTCT GTGACTGGTG  
4851 AGTACTCAAC CAAGTCATTC TGAGAATAGT GTATGCGGCG ACCGAGTTGC  
4901 TCTTGCCCGG CGTCAACACG GGATAATACC GCGCCACATA GCAGAACTTT  
4951 AAAAGTGCTC ATCATTGGAA AACGTTCTTC GGGGCGAAAA CTCTCAAGGA  
5001 TCTTACCGCT GTTGAGATCC AGTTCGATGT AACCCACTCG TGCACCCAAC  
5051 TGATCTTCAG CATCTTTTAC TTTCAACCAGC GTTTCTGGGT GAGCAAAAAC  
5101 AGGAAGGCAA AATGCCGCAA AAAAGGGAAT AAGGGCGACA CGGAAATGTT  
5151 GAATACTCAT ACTCTTCCTT TTTCAATATT ATTGAAGCAT TTATCAGGGT  
5201 TATTGTCTCA TGAGCGGATA CATATTTGAA TGTATTTAGA AAAATAAACA  
5251 AATAGGGGTT CCGCGCACAT TTCCCCGAAA AGTGCCACCT GACGTCTAAG  
5301 AAACCATTAT TATCATGACA TTAACCTATA AAAATAGGCG TATCAGGAGG  
5351 CCCTTTCGTC TTCAA

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# FIG. 20

pBG396  
 :BG368 backbone  
 :soluble T4#12  
 :AA #3 = LYS

bg396:seq Length: 5518

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1  GAATTAATTC CAGCTTGCTG TGGAATGTGT GTCAGTTAGG GTGTGGAAAG
51  TCCCCAGGCT CCCCAGCAGG CAGAAGTATG CAAAGCATGC ATCTCAATTA
101 GTCAGCAACC AGGTGTGGAA AGTCCCCAGG CTCCCCAGCA GGCAGAAGTA
151 TGCAAAGCAT GCATCTCAAT TAGTCAGCAA CCATAGTCCC GCCCCTAACT
201 CCGCCCATCC CGCCCCTAAC TCCGCCCAGT TCCGCCCATT CTCCGCCCCA
251 TGGCTGACTA ATTTTTTTTA TTTATGCAGA GGCCGAGGCC GCCTCGGCCT
301 CTGAGCTATT CCAGAAGTAG TGAGGAGGCT TTTTGGAGG GGTCCTCCTC
351 GTATAGAAAC TCGGACCACT CTGAGACGAA GGCTCGCGTC CAGGCCAGCA
401 CGAAGGAGGC TAAGTGGGAG GGGTAGCGGT CGTTGTCCAC TAGGGGGTCC
451 ACTCGCTCCA GGGTGTGAAG ACACATGTCT CCTCTTCGG CATCAAGGAA
501 GGTGATTGGT TTATAGGTGT AGGCCACGTG ACCGGGTGTT CCTGAAGGGG
551 GGCTATAAAA GGGGGTGGGG GCGCGTTCGT CCTCACTCTC TTCCGCATCG
601 CTGTCTGCGA GGGCCAGCTG TTGGGCTCGC GGTTGAGGAC AAACCTCTTCG
651 CGGTCTTTCC AGTACTCTTG GATCGGAAAC CCGTCGGCCT CCGAACGGTA
701 CTCCGCCACC GAGGGACCTG AGCGAGTCCG CATCGACCGG ATCGGAAAAAC
751 CTCTCGAGAA AGGCGTCTAA CCAGTCACAG TCGCAAGGTA GGCTGAGCAC
801 CGTGGCGGGC GGCAGCGGGT GGCGGTCTGGG GTTGTTTCTG GCGGAGGTGC
851 TGCTGATGAT GTAATTAAAG TAGGCGGTCT TGAGACGGCG GATGGTCGAG
901 GTGAGGTGTG GCAGGCTTGA GATCGATCTG GCCATACACT TGAGTGACAA
951 TGACATCCAC TTTGCCTTTC TCTCCACAGG TGTCCACTCC CAGGTCCAAC
1001 TGGATCCAAG CTTCGACTCG AGGAATTCCC CGAAGGAACA AAGCACCCCTC
1051 CCCACTGGGC TCCTGGTTGC AGAGCTCCAA GTCTCACAC AGATACGCCT
1101 GTTTGAGAAG CAGCGGGCAA GAAAGACGCA AGCCCAGAGG CCCTGCCATT
1151 TCTGTGGGCT CAGGTCCCTA CTGGCTCAGG CCCCTGCCTC CCTCGGCAAG
1201 GCCACAATGA ACCGGGGAGT CCCTTTTAGG CACTTGCTTC TGGTGCTGCA
1251 ACTGGCGCTC CTCCCAGCAG CCACTCAGGG AAAGAAAGTG GTGCTGGGCA
1301 AAAAAGGGGA TACAGTGGAA CTGACCTGTA CAGCTTCCCA GAAGAAGAGC
1351 ATACAATTCC ACTGGAAGAA CTGCAACCAG ATAAAGATTC TGGGAAATCA
1401 GGGCTCCTTC TTAATAAAG GTCCATCCAA GCTGAATGAT CGCGCTGACT
  
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## FIG. 20 (cont'd)

1451 CAAGAAGAAG CTTGTGGGAC CAAGGAAACT TTCCCCTGAT CATCAAGAAT  
1501 CTTAAGATAG AAGACTCAGA TACTTACATC TGTGAAGTGG AGGACCAGAA  
1551 GGAGGAGGTG CAATTGCTAG TGTTCGGATT GACTGCCAAC TCTGACACCC  
1601 ACCTGCTTCA GGGGCAGAGC CTGACCCTGA CCTTGGAGAG CCCCCCTGGT  
1651 AGTAGCCCCCT CASTGCAATG TAGGAGTCCA AGGGGTAAAA ACATACAGGG  
1701 GGGGAAGACC CTCTCCCTGT CTCAGCTGGA GCTCCAGGAT AGTGGCACCT  
1751 GGACATGCAC TGTCTTGCAG AACTGAGATC TTTGTGAAGG AACCTTACTT  
1801 CTGTGGTGTG ACATAATTGG ACAAACCTACC TACAGAGATT TAAAGCTCTA  
1851 AGGTAAATAT AAAATTTTAA AGTGTATAAT GTGTAAACT ACTGATTCTA  
1901 ATTGTTTGTG TATTTTAGAT TCCAACCTAT GGAAGTATG AATGGGAGCA  
1951 GTGGTGAAT GCCTTTAATG AGGAAAACCT GTTTTGCTCA GAAGAAATGC  
2001 CATCTAGTGA TGATGAGGCT ACTGCTGACT CTCAACATTC TACTCCTCCA  
2051 AAAAAGAAGA GAAAGGTAGA AGACCCCAAG GACTTTCCTT CAGAATTGCT  
2101 AAGTTTTTTG AGTCATGCTG TGTTTAGTAA TAGAACTCTT GCTTGCTTTG  
2151 CTATTTACAC CACAAAGGAA AAAGCTGCAC TGCTATACAA GAAAATTATG  
2201 GAAAAATATT CTGTAACCTT TATAAGTAGG CATAACAGTT ATAATCATAA  
2251 CATACTGTTT TTTCTTACTC CACACAGGCA TAGAGTGTCT GCTATTAATA  
2301 ACTATGCTCA AAAATTGTGT ACCTTTAGCT TTTTAATTTG TAAAGGGGTT  
2351 AATAAGGAAT ATTTGATGTA TAGTGCCTTG ACTAGAGATC ATAATCAGCC  
2401 ATACCACATT TGTAGAGGTT TTACTTGCTT TAAAAAACCT CCCACACCTC  
2451 CCCCTGAACC TGAAACATAA AATGAATGCA ATTGTTGTTG TTAAGTTGTT  
2501 TATTGCAGCT TATAATGGTT ACAAATAAAG CAATAGCATC ACAAATTTCA  
2551 CAAATAAAGC ATTTTTTTCA CTGCATTCTA GTTGTGGTTT GTCCAAACTC  
2601 ATCAATGTAT CTTATCATGT CTGGATCCTC TACGCCGGAC GCATCGTGGC  
2651 CGGCATCACC GCGCCACAG GTGCGGTTGC TGGCGCCTAT ATCGCCGACA  
2701 TCACCGATGG GGAAGATCGG GCTCGCCACT TCGGGCTCAT GAGCGCTTGT  
2751 TTCGCGTGG GTATGGTGGC AGGCCCGTGG CCGGGGGACT GTTGGGCGCC  
2801 ATCTCTTGC ATGCACCATT CCTTGCGGCG GCGGTGCTCA ACGGCCTCAA  
2851 CCTACTACTG GGCTGCTTCC TAATGCAGGA GTCGCATAAG GGAGAGCGTC  
2901 GACCGATGCC CTTGAGAGCC TTCAACCCAG TCAGCTCCTT CCGGTGGGCG  
2951 CGGGGCATGA CTATCGTCGC CGCACTTATG ACTGTCTTCT TTATCATGCA  
3001 ACTCGTAGGA CAGGTGCTGCTG GGTCAATTTT CCGGAGGACC  
3051 GCTTTGCTG GAGCGGACG ATGATCGGCC TGTCGCTTGC GGTATTCGGA

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## FIG. 20 (cont'd)

3101 ATCTTGCAAG CCCTCGCTCA AGCCTTCGT ACTGGTCCCG CCACCAAACG  
3151 TTTCGGCGAG AAGCAGGCCA TTATCGCCGG CATGGCGGCC GACGCGCTGG  
3201 GCTACGTCTT GCTGGCGTTC GCGACGCGAG GCTGGATGGC CTTCGCCATT  
3251 ATGATTCTTC TCGCTTCCGG CGGCATCGGG ATGCCCGCGT TGCAGGCCAT  
3301 GCTGTCCAGG CAGGTAGATG ACGACCATCA GGGACAGCTT CAAGGATCGC  
3351 TCGCGGCTCT TACCAGCCTA ACTTCGATCA CTGGACCGCT GATCGTCACG  
3401 GCGATTTATG CCGCCTCGGC GAGCACATGG AACGGGTTGG CATGGATTGT  
3451 AGGCGCCGCC CTATACCTTG TCTGCCTCC CCGTTGCGT CGCGGTGCAT  
3501 GGAGCCGGGC CACCTCGACC TGAATGGAAG CCGGCGGCAC CTCGCTAACG  
3551 GATTCACCAC TCCAAGAATT GGAGCCAA<sup>T</sup>C AATTCTTGCG GAGAACTGTG  
3601 AATGCGCAAA CCAACCCTTG GCAGAACATA TCCATCGCGT CCGCCATCTC  
3651 CAGCAGCCGC ACGCGGCGCA TCTCGGGCCG CGTTGCTGGC GTTTTTCCAT  
3701 AGGCTCCGCC CCCCTGACGA GCATCACAAA AATCGACGCT CAAGTCAGAG  
3751 GTGGCGAAAC CCGACAGGAC TATAAGATA CCAGGCGTTT CCCCCTGGAA  
3801 GCTCCCTCGT GCGCTCTCT GTTCCGACCC TGCCGCTTAC CGGATACCTG  
3851 TCCGCCTTTC TCCCTTCGGG AAGCGTGGCG CTTTCTCAAT GCTCAGCTG  
3901 TAGGTATCTC AGTTCGGTGT AGGTCGTTTG CTCCAAGCTG GGCTGTGTGC  
3951 ACGAACCCCC CGTTCAGCCC GACCGCTGCG CTTATCCGG TAACTATCGT  
4001 CTTGAGTECA ACCCGGTAAG ACACGACTTA TCGCCACTGG CAGCAGCCAC  
4051 TGGTAACAGG ATTAGCAGAG CGAGGTATGT AGGCGGTGCT ACAGAGTTCT  
4101 TGAAGTGGTG GCCTAACTAC GGCTACACTA GAAGGACAGT ATTTGGTATC  
4151 TGCGCTCTGC TGAAGCCAGT TACCTTCGGA AAAAGAGTTG GTAGCTCTTG  
4201 ATCCCGCAAA CAAACCACCG CTGGTAGCGG TGGTTTTTTT GTTTGCAAGC  
4251 AGCAGATTAC GCGCAGAAAA AAAGGATCTC AAGAAGATCC TTTGATCTTT  
4301 TCTACGGGGT CTGACGCTCA GTGGAACGAA AACTCACGTT AAGGGATTTT  
4351 GGTGATGAGA TTATCAAAAA GGATCTTCAC CTAGATCCTT TAAATTA  
4401 AATGAAGTTT TAAATCAATC TAAAGTATAT ATGAGTAAAC TTGGTCTGAC  
4451 AGTTACCAAT GCTTAATCAG TGAGGCACCT ATCTCAGCGA TCTGTCTATT  
4501 TCGTTCATCC ATAGTTGCCT GACTCCCCGT CGTGTAGATA ACTACGATAC  
4551 GGGAGGGCTT ACCATCTGGC CCCAGTGCTG CAATGATACC GCGAGACCCA  
4601 CGCTACCGG CTCCAGATTT ATCAGCAATA AACCAGCCAG CCGGAAGGGC  
4651 CGAGCGCAGA AGTGGTCTC<sup>T</sup>CAACTTTATC CGCCTCCATC CAGTCTATTA  
3701 ATCTTCCCG GGAAGCTAGA GTAAGTAGTT CGCCAGTTAA TAGTTTGCGC  
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# FIG. 20 (cont'd)

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4751 AACGTTGTTG CCATTGCTGC AGGCATCGTG GTGTCACGCT CGTCGTTTGG
4801 TATGGCTTCA TTCAGCTCCG GTTECCAACG ATCAAGGCGA GTTACATGAT
4851 CCCCCATGTT GTGCAAAAAA GCGGTTAGCT CCTTCGGTCC TCCGATCGTT
4901 GTCAGAAGTA AGTTGGCCGC AGTGTTATCA CTCATGGTTA TGGCAGCACT
4951 GCATAATTCT CTTACTGTCA TGCCATCCGT AAGATGCTTT TCTGTGACTG
5001 GTGAGTACTC AACCAAGTCA TTCTGAGAAT AGTGTATGCG GCGACCGAGT
5051 TGCTCTTGCC CGGCGTCAAC ACGGGATAAT ACCGCGCCAC ATAGCAGAAC
5101 TTTAAAAGTG CTCATCATTG GAAAACGTTC TTCGGGGCGA AAACCTCTCA
5151 GGATCTTACC GCTGTTGAGA TCCAGTTCGA TGTAACCCAC TCGTGACCCC
5201 AACTGATCTT CAGCATCTTT TACTTTCACC AGCGTTTCTG GGTGAGCAAA
5251 AACAGGAAGG CAAAATGCCG CAAAAAAGGG AATAAGGGCG ACACGGAAAT
5301 GTTGAATACT CATACTCTTC CTTTTTCAAT ATTATTGAAG CATTATCAG
5351 GGTtATTGTC TCATGAGCGG ATACATATTT GAATGTATTT AGAAAAATAA
5401 ACAAATAGGG GTTCCGCGCA CATTTCCTCCG AAAAGTGCCA CCTGACGTCT
5451 AAGAAACCAT TATTATCATG ACATTAACCT ATAAAAATAG GCGTATCAG
5501 AGGCCCTTTC GTCTTCAA

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PBQ393  
 :BG368 backbone  
 :soluble T4#8  
 :AA #3 = LVS  
 : "perfect" Stu/first 182 AA of T4  
 : basically up to V2J2

FIG. 21

bg393.seq Length: 5566

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1  GAATTAATTC CAGCTTGCTG TGAATGTGT GTCAGTTAGG GTGTGGAAAG
51  TCCCCAGGCT CCCCAGCAGG CAGAAGTATG CAAAGCATGC ATCTCAATTA
101 GTCAGCAACC AGGTGTGGAA AGTCCCCAGG CTCCCCAGCA GGCAGAAGTA
151 TGCAAAGCAT GCATCTCAAT TAGTCAGCAA CCATAGTCCC GCCCCTAACT
201 CCGCCCATCC CGCCCCTAAC TCCGCCCAGT TCCGCCCATT CTCCGCCCCA
251 TGGCTGACTA ATTTTTTTTA TTTATGCAGA GGCCGAGGCC GCCTCGGCCT
301 CTGAGCTATT CCAGAAGTAG TGAGGAGGCT TTTTGGAGG GGTCCTCCTC
351 GTATAGAAAC TCGGACCACT CTGAGACGAA GGCTCGCGTC CAGGCCAGCA
401 CGAAGGAGGC TAAGTGGGAG GGGTAGCGGT CGTTGTCCAC TAGGGGGTCC
451 ACTCGCTCCA GGGTGTGAAG ACACATGTCT CCCTCTTCGG CATCAAGGAA
501 GGTGATTGGT TTATAGGTGT AGGCCACGTG ACCGGGTGTT CCTGAAGGGG
551 GGCTATAAAA GGGGGTGGGG GCGCGTTCGT CCTCACTCTC TTCCGCATCG
601 CTGTCTGCGA GGGCCAGCTG TTGGGCTCGC GGTTGAGGAC AAACCTCTTCG
651 CGGTCTTTCC AGTACTCTTG GATCGGAAAC CCGTCGGCCT CCGAACGGTA
701 CTCCGCCACC GAGGGACCTG AGCGAGTCCG CATCGACCGG ATCGGAAAAC
751 CTCTCGAGAA AGGCGTCTAA CCAGTCACAG TCGCAAGGTA GGCTGAGCAC
801 CGTGGCGGGC GGCAGCGGGT GGCGGTCGGG GTTGTTTCTG GCGGAGGTGC
851 TGCTGATGAT GTAATTAAAG TAGGCGGTCT TGAGACGGCG GATGGTCGAG
901 GTGAGGTGTG GCAGGCTTGA GATCGATCTG GCCATACACT TGAGTGACAA
951 TGACATCCAC TTTGCCTTTC TCTCCACAGG TGTCCACTCC CAGGTCCAAC
1001 TGGATCCAAG CTTGCACTCG AGGAATTCCC CGAAGGAACA AAGCACCCCTC
1051 CCCACTGGGC TCCTGGTTGC AGAGCTCCAA GTCCTCACAC AGATACGCCT
1101 GTTTGAGAAG CAGCGGGCAA GAAAGACGCA AGCCCAGAGG CCCTGCCATT
1151 TCTGTGGGCT CAGGTCCCTA CTGGCTCAGG CCCCTGCCTC CCTCGGCAAG
1201 GCCACAATGA ACCGGGGAGT CCCTTTTAGG CACTTGCTTC TGGTGCTGCA
1251 ACTGGCGCTC CTCCAGCAG CCACTCAGGG AAAGAAAGTG GTGCTGGGCA
1301 AAAAAGGGGA TACAGTCCAA CTGACCTGTA CAGCTTCCCA GAAGAAGAGC
1351 ATACAATTCC ACTGGAAAAA CTCCAACCAG ATAAAGATTC TGGGAAATCA

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## FIG. 21 (cont'd)

1401 GGGCTCCTTC TTAACATAAG GTCCATCCAA GCTGAATGAT CGCGCTGACT  
 1451 CAAGAAGAAG CTTGTGGGAC CAAGGAAACT TTCCCTGAT CATCAAGAAT  
 1501 CTTAAGATAG AAGACTCAGA TACTTACATC TGTGAAGTGG AGGACCAGAA  
 1551 GGAGGAGGTG CAATTGCTAG TGTTCGGATT GACTGCCAAC TCTGACACCC  
 1601 ACCTGCTTCA GGGGCAGAGC CTGACCCTGA CCTTGGAGAG CCCCCCTGGT  
 1651 AGTAGCCCCCT CAGTGCAATG TAGGAGTCCA AGGGGTAAAA ACATACAGGG  
 1701 GGGGAAGACC CTCTCCGTGT CTCAGCTGGA GCTCCAGGAT AGTGGCACCT  
 1751 GGACATGCAC TGTCTTGCAG AACCAGAAGA AGGTGGAGTT CAAAATAGAC  
 1801 ATCGTGGTGC TAGCTTTCCA GTGAGATCTT TGTGAAGGAA CCTTACTTCT  
 1851 GTGGTGTGAC ATAATTGGAC AAACACCTA CAGAGATTTA AAGCTCTAAG  
 1901 GTAAATATAA AATTTTAAAG TGTATAATGT GTTAACTAC TGATTCTAAT  
 1951 TGTTTGTGTA TTTTAGATTG CAACCTATGG AACTGATGAA TGGGAGCAGT  
 2001 GGTGGAATGC CTTTAATGAG GAAAACCTGT TTTGCTCAGA AGAAATGCCA  
 2051 TCTAGTGATG ATGAGGCTAC TGCTGACTCT CAACATTCTA CTCCTCCAAA  
 2101 AAAGAAGAGA AAGGTAGAAG ACCCCAAGGA CTTTCCTTCA GAATTGCTAA  
 2151 GTTTTTTGAG TCATGCTGTG TTTAGTAATA GAACTCTTGC TTGCTTTGCT  
 2201 ATTTACACCA CAAAGGAAAA AGCTGCACTG CTATACAAGA AAATTATGGA  
 2251 AAAATATTCT GTAACCTTTA TAAGTAGGCA TAACAGTTAT AATCATAACA  
 2301 TACTGTTTTT TCTTACTCCA CACAGGCATA GAGTGTCTGC TATTAATAAC  
 2351 TATGCTCAAA AATTGTGTAC CTTTAGCTTT TTAATTTGTA AAGGGGTAA  
 2401 TAAGGAATAT TTGATGTATA GTGCCTTGAC TAGAGATCAT AATCAGCCAT  
 2451 ACCACATTTG TAGAGGTTTT ACTTGCTTTA AAAAACCTCC CACACCTCCC  
 2501 CCTGAACCTG AAACATAAAA TGAATGCAAT TGTGTTGTT AACTTGTTTA  
 2551 TTGCAGCTTA TAATGGTTAC AAATAAAGCA ATAGCATCAC AAATTTTACA  
 2601 AATAAAGCAT TTTTTTCACT GCATTCTAGT TGTGGTTTGT CCAAACATCAT  
 2651 CAATGTATCT TATCATGTCT GGATCCTCTA CGCCGGACGC ATCGTGGCCG  
 2701 GCATCACCGG CGCCACAGGT GCGGTTGCTG GCGCCTATAT CGCCGACATC  
 2751 ACCGATGGGG AAGATCGGGC TCGCCACTTC GGGCTCATGA GCGCTTGTTT  
 2801 CGGCGTGGGT ATGGTGGCAG GCCCGTGGCC GGGGGACTGT TGGGCGCCAT  
 2851 CTCCTTGCAAT GCACCATTCCT TTGCGGCGGC GGTGCTCAAC GGCCTCAACC  
 2901 TACTACTGGG CTGCTTCCTA ATGCAGGAGT CGCATAAGGG AGAGCGTCCA  
 2951 CCGATGCCCT TGAGAGCTTT GAACCGAGTC AGCTCCTTCC GGTGGGCGCG  
 3001 GGGCATGACT ATCGTCGCGG CACTTATGAC TGTCTTCTTT ATCATGCAAC

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*FIG. 21 (cont'd)*

3051 TCGTAGGACA GGTGCCGGCA GCGCTCTGGG TCATTTTCGG CGAGGACCGC  
3101 TTTCGCTGGA GCGCGACGAT GATCGGCCCG TCGCTTGCGG TATTCGGAAT  
3151 CTTGCACGCC CTCGCTCAAG CCTTCGTAC TGGTCCCGCC ACCAAACGTT  
3201 TCGGCGAGAA GCAGGCCATT ATCGCCGGCA TGGCGGCCGA CGCGCTGGGC  
3251 TACGTCTTGC TGGCGTTTCG GACGCGAGGC TGGATGGCCT TCCCCATTAT  
3301 GATTCTTCTC GCTTCCGGCG GCATCGGGAT GCCCGCGTTG CAGGCCATGC  
3351 TGTCCAGGCA GGTAGATGAC GACCATCAGG GACAGCTTCA AGGATCGCTC  
3401 GCGGCTCTTA CCAGCCTAAC TTCGATCACT GGACCGCTGA TCGTCACGGC  
3451 GATTTATGCC GCCTCGGCGA GCACATGGAA CGGGTTGGCA TGGATTGTAG  
3501 GCGCCGCCCT ATACCTTGTC TGCTCCCCG CGTTGCGTCG CGGTGCATGG  
3551 AGCCGGGCCA CCTCGACCTG AATGGAAGCC GGCGGCACCT CGCTAACGGA  
3601 TTCACCACTC CAAGAATTGG AGCCAATCAA TTCTTGCGGA GAACTGTGAA  
3651 TGGCGAAACC AACCCTTGGC AGAACATATC CATCGCGTCC GCCATCTCCA  
3701 GCAGCCGCAC GCGGCGCATC TCGGGCCGCG TTGCTGGCGT TTTTCCATAG  
3751 GCTCCGCCCC CCTGACGAGC ATCACAAAAA TCGACGCTCA AGTCAGAGGT  
3801 GGCgAAACCC GACAGGACTA TAAAGATACC AGGCGTTTCC CCCTGGAAGC  
3851 TCCCTCGTGC GCTCTCCTGT TCCGACCCTG CCGCTTACCG GATACCTGTC  
3901 CGCCTTTCTC CCTTCGGGAA GCGTGGCGCT TTCTCAATGC TCACGCTGTA  
3951 GGTATCTCAG TTCGGTGTAG GTCGTTGCT CCAAGCTGGG CTGTGTGCAC  
4001 GAACCCCCCG TTCAGCCCGA CCGCTGCGCC TTATCCGGTA ACTATCGTCT  
4051 TGAGTCCAAC CCGGTAAGAC ACGACTTATC GCCACTGGCA GCAGCCACTG  
4101 GTAACAGGAT TAGCAGAGCG AGGTATGTAG GCGGTGCTAC AGAGTTCTTG  
4151 AAGTGGTGGC CTAACACGG CTACACTAGA AGGACAGTAT TTGGTATCTG  
4201 CGCTCTGCTG AAGCCAGTTA CCTTCGGAAA AAGAGTTGGT AGCTCTTGAT  
4251 CCGGCAAACA AACCACCGCT GGTAGCGGTG GTTTTTTTGT TTGCAAGCAG  
4301 CAGATTACGC GCAGAAAAAA AGGATCTCAA GAAGATCCTT TGATCTTTTC  
4351 TACGGGGTCT GACGCTCAGT GGAACGAAAA CTCACGTAA GGGATTTTGG  
4401 TCATGAGATT ATCAAAAAGG ATCTTCACCT AGATCCTTTT AAATTAAAAA  
4451 TGAAGTTTTA AATCAATCTA AAGTATATAT GAGTAACTT GGTCTGACAG  
4501 TTACCAATGC TTAATCAGTG AGGCACCTAT CTCAGCGATC TGTCTATTTT  
4551 GTTCATCCAT AGTTGCCTGA CTCCCCGTCT TGTAGATAAC TACGATACGG  
4601 GAGGGCTTAC CATCTGGCCC CAGTGTGCA ATGATACCGC GAGACCCACG  
4651 CTCACCGGCT CCAGATTTAT CAGCAATAAA CCAGCCAGCC GGAAGGGCCG

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*FIG. 21 (cont'd)*

4701 AGCGCAGAAG TGGTCCTGCA ACTTTATCCG CCTCCATCCA GTCTATTAAT  
4751 TGTTGCCGGG AAGCTAGAGT AAGTAGTTCG CCAGTTAATA GTTTGCGCAA  
4801 CGTTGTTGCC ATTGCTGCAG GCATCGTGGT GTCACGCTCG TCGTTTGGTA  
4851 TGGCTTCATT CAGCTCCGGT TCCCAACGAT CAAGGCGAGT TACATGATCC  
4901 CCCATGTTGT GCAAAAAAGC GGTAGCTCC TTCGGTCCTC CGATCGTTGT  
4951 CAGAAGTAAG TTGGCCGCAG TGTTATCACT CATGGTTATG GCAGCACTGC  
5001 ATAATTCTCT TACTGTCATG CCATCCGTAA GATGCTTTTC TGTGACTGGT  
5051 GAGTACTCAA CCAAGTCATT CTGAGAATAG TGTATGCGGC GACCGAGTTG  
5101 CTCTTGCCCG GCGTCAACAC GGGATAATAC CGCGCCACAT AGCAGAACTT  
5151 TAAAAGTGCT CATCATTGGA AAACGTTCTT CGGGGCGAAA ACTCTCAAGG  
5201 ATCTTACCGC TGTTGAGATC CAGTTCGATG TAACCCACTC GTGCACCCAA  
5251 CTGATCTTCA GCATCTTTTA CTTTCACCAG CGTTTCTGGG TGAGCAAAAA  
5301 CAGGAAGGCA AAATGCCGCA AAAAAGGGAA TAAGGGCGAC ACGGAAATGT  
5351 TGAATACTCA TACTCTTCCT TTTTCAATAT TATTGAAGCA TTTATCAGGG  
5401 TTATTGTCTC ATGAGCGGAT ACATATTTGA ATGTATTTAG AAAAATAAAC  
5451 AAATAGGGGT TCCGCGCACA TTTCCCCGAA AAGTGCCACC TGACGTCTAA  
5501 GAAACCATTA TTATCATGAC ATTAACCTAT AAAAATAGGC GTATCACGAG  
5551 GCCCTTTCGT CTTCAA

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P8G395  
 :BG368 backbone  
 :soluble T4#10  
 :AA #3 = LVS  
 :first 131 AA of T4

bg395.seq Length 5413

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: GAATTAATTC CAGCTTGCTG TGGAAATGTGT GTCAGTTAGG GTGTGGAAAG
51 TCCCCAGGCT CCCCAGCAGG CAGAAGTATG CAAAGCATGC ATCTCAATTA
101 GTCAGCAACC AGGTGTGGAA AGTCCCCAGG CTCCCCAGCA GGCAGAAGTA
151 TGCAAAGCAT GCATCTCAAT TAGTCAGCAA CCATAGTCCC GCCCCTAACT
201 CCGCCCATCC CGCCCCTAAC TCCGCCCAGT TCCGCCCATT CTCGCCCCCA
251 TGGCTGACTA ATTTTTTTTA TTTATGCAGA GGCCGAGGCC GCCTCGGCCT
301 CTGAGCTATT CCAGAAGTAG TGAGGAGGCT TTTTGGAGG GGTCCTCCTC
351 GTATAGAAAC TCGGACCACT CTGAGACGAA GGCTCGCGTC CAGGCCAGCA
401 CGAAGGAGGC TAAGTGGGAG GGGTAGCGGT CGTTGTCCAC TAGGGGGTCC
451 ACTCGCTCCA GGGTGTGAAG ACACATGTCT CCCTCTTCGG CATCAAGGAA
501 GGTGATTGGT TTATAGGTGT AGGCCACGTG ACCGGGTGTT CCTGAAGGGG
551 GGCTATAAAA GGGGGTGGGG GCGCGTTCGT CCTCACTCTC TTCCGCATCG
601 CTGTCTGCGA GGGCCAGCTG TTGGGCTCGC GGTTGAGGAC AAACCTCTCG
651 CGGTCTTTCC AGTACTCTTG GATCGGAAAC CCGTCGGCCT CCGAACGGTA
701 CTCCGCCACC GAGGGACCTG AGCGAGTCCG CATCGACCGG ATCGGAAAAC
751 CTCTCGAGAA AGGCGTCTAA CCAGTCACAG TCGCAAGGTA GGCTGAGCAC
801 CGTGGCGGGC GGCAGCGGGT GGCGGTCTGG GTTGTCTCTG GCGGAGGTGC
851 TGCTSATGAT GTAATTAAAG TAGGCGGTCT TGAGACGGCG GATGGTCGAG
901 GTGAGGTGTG GCAGGLTTGA GATCGATCTG GCCATACACT TGAGTGACAA
951 TGACATCCAC TTGCTTTTC TCTCCACAGG TGTCCTCTCC CAGGTCCAA-
1001 TGGATCCAAG CTTCGACTCG AGGAATTCCC CGAAGGAACA AAGCACCTC
1051 CCCACTGGGC TCCTGGTTGC AGAGCTCCAA GTCCTCACAC AGATACGCCT
1101 GTTTGAGAAG CAGCGGGCAA GAAAGACGCA AGCCCAGAGG CCCTGCCATT
1151 TCTGTGGGCT CAGGTCCCTA CTGGCTCAGG CCCCTGCCTC CCTCGGCAAG
1201 GCCACAATGA ACCGGGGAGT CCCTTTTAGG CACTTGCTTC TGGTGCTGCA
1251 ACTGGCGCTC CTCCCAGCAG CCACTCAGGG AAAGAAAGTG GTGCTGGGCA
1301 AAAAAGGGGA TACAGTGGAA CTGACCTGTA CAGCTTCCCA GAAGAAGAGC
1351 ATACAATTCC ACTGGAAAAA CTCCAACCAG ATAAAGATTG TGGGAAATCA
1401 GGGCTCCTTC TTAACATAAG GTCCATCCAA GCTGAATGAT CGCGCTGACT
  
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SEQUENCE SHEET

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FIG. 22(cont'd)

1451 CAAGAAGAAG CTTGTGGGAC CAAGGAAACT TTCCCCTGAT CATCAAGAAT  
1501 CTTAAGATAG AAGACTCAGA TACTTACATC TGGAAGTGG AGGACCAGAA  
1551 GGAGGAGGTG CAATTGCTAG TGTTCGGATT GACTGCCAAC TCTGACACCC  
1601 ACCTGCTTCA GGGGCAGAGC CTGACCCTGA CTTTGGAGAG CCCCCCGGGT  
1651 AGTAGCCCCT CAGTGCAATG AGATCTTTGT GAAGGAACCT TACTTCTGTG  
1701 GTGTGACATA ATTGGACAAA CTACCTACAG AGATTTAAAG CTCTAAGGTA  
1751 AATATAAAAT TTTTAAGTGT ATAATGTGTT AAACACTGTA TTCTAATTGT  
1801 TTGTGTATTT TAGATTCCAA CCTATGGAAC TGATGAATGG GAGCAGTGGT  
1851 GGAATGCCTT TAATGAGGAA AACCTGTTTT GCTCAGAAGA AATGCCATCT  
1901 AGTGATGATG AGGCTACTGC TGA CTCTCAA CATTCTACTC CTCCAAAAAA  
1951 GAAGAGAAAG GTAGAAGACC CCAAGGACTT TCCTTCAGAA TTGCTAAGTT  
2001 TTTTGAGTCA TGCTGTGTTT AGTAATAGAA CTCTTGCTTG CTTTGCTATT  
2051 TACACCACAA AGGAAAAAGC TGA CTGCTA TACAAGAAAA TTATGGAAAA  
2101 ATATTCTGTA ACCTTTATAA GTAGGCATAA CAGTTATAAT CATAACATAC  
2151 TGT TTTTCT TACTCCACAC AGGCATAGAG TGTCTGCTAT TAATAACTAT  
2201 GCTCAAAAAT TGTGTACCTT TAGCTTTTTTA ATTTGTAAAG GGGTTAATAA  
2251 GGAATATTTG ATGTATAGTG CTTGACTAG AGATCATAAT CAGCCATACC  
2301 ACATTTGTAG AGGTTTTACT TGCTTTAAAA AACCTCCAC ACCTCCCCCT  
2351 GAACCTGAAA CATAAAATGA ATGCAATTGT TGTGTTAAC TTGTTTATTG  
2401 CAGCTTATAA TGGTTACAAA TAAAGCAATA GCATCACAAA TTTCACAAAT  
2451 AAAGCATTTT TTTCACTGCA TTCTAGTTGT GGTTTGTTCA AACTCATCAA  
2501 TGTATCTTAT CATGTCTGGA TCCTCTACGC CGGACGCATC GTGGCCGGCA  
2551 TCACCGGCGC CACAGGTGCG GTTGCTGGCG CCTATATCGC CGACATCACC  
2601 GATGGGGAAG ATCGGGCTCG CCACTTCGGG CTCATGAGCG CTTGTTTCGG  
2651 CGTGGGTATG GTGGCAGGCC CGTGGCCGGG GGA CTGTTGG GCGCCATCTC  
2701 CTTGCATGCA CCATTCCTTG CGGCGGCGGT GCTCAACGGC CTCAACCTAC  
2751 TACTGGGCTG CTTCTTAATG CAGGAGTCGC ATAAGGGAGA GCGTCGACCG  
2801 ATGCCCTTGA GAGCCTTCAA CCCAGTCAGC TCCTTCGGT GGGCGCGGGG  
2851 CATGACTATC GTCGCCGCAC TTATGACTGT CTTCTTTATC ATGCAACTCG  
2901 TAGGACAGGT GCCGGCAGCG CTCTGGGTCA TTTTCGGCGA GGACCGCTTT  
2951 CGCTGGAGCG CGACGATGAT CGGCCTGTG CTTGCGGTAT TCGGAATCTT  
3001 GCACGCGCTC GCTCAAGCCT TCGTCACTGG TCCCGCCACC AAACGTTTCG  
3051 GCGAGAAGCA GCGCTTTA GCGGCGCATGG CGGCCGACGC GCTGGGCTAC

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## FIG. 22(cont'd)

3101 GTCTTGCTGG CGTTCGCGAC CCGAGGCTGG ATGGCCTTCC CCATTATGAT  
3151 TCTTCTCGCT TCCGGCGGCA TCGGGATGCC CGCGTTGCAG GCCATGCTGT  
3201 CCAGGCAGGT AGATGACGAC CATCAGGGAC AGCTTCAAGG ATCGCTCGCG  
3251 GCTCTTACCA GCCTAACTTC GATCACTGGA CCGCTGATCG TCACGGCGAT  
3301 TTATGCCGCG TCGGCGAGCA CATGGAACGG GTTGGCATGG ATTGTAGGCG  
3351 CCGCCCTATA CCTTGTCTGC CTCCCCGCGT TCGCTCGCGG TGCATGGAGC  
3401 CGGGCCACCT CGACCTGAAT GGAAGCCGGC GGLACCTCGC TAACGGATTC  
3451 ACCACTCCAA GAATTGGAGC CAATCAATTC TTGCGGAGAA CTGTGAATGC  
3501 GCAAACCAAC CCTTGGCAGA ACATATCCAT CGCGTCCGCC ATCTCCAGCA  
3551 GCCGCACGCG GCGCATCTCG GGCCGCGTTG CTGGCGTTTT TCCATAGGCT  
3601 CCGCCCCCTT GACGAGCATC AAAAAATCG ACGCTCAAGT CAGAGGTGGC  
3651 GAAACCCGAC AGGACTATAA AGATACCAGG CGTTTCCCCC TGGAAAGCTCC  
3701 CTCGTGCGCT CTCCTGTTCC GACCCTGCCG CTTACCGGAT ACCTGTCCGC  
3751 CTTTCTCCCT TCGGGAAGCG TGGCGCTTTC TCAATGCTCA CGCTGTAGGT  
3801 ATCTCAGTTC GGTGTAGGTC GTTCGCTCCA AGCTGGGCTG TGTGCACGAA  
3851 CCCCCCGTTC AGCCCGACCG CTGCGCCTTA TCCGGTAACT ATCGTCTTGA  
3901 GTCCAACCCG GTAAGACACG ACTTATCGCC ACTGGCAGCA GCCACTGGTA  
3951 ACAGGATTAG CAGAGCGAGG TATGTAGGCG GTGCTACAGA GTTCTTGAAG  
4001 TGGTGGCCTA ACTACGGCTA CACTAGAAGG ACAGTATTTG GTATCTGCGC  
4051 TCTGCTGAAG CCAGTTACCT TCGGAAAAAG AGTTGGTAGC TCTTGATCCG  
4101 GCAAAACAAAC CACCGCTGGT AGCGGTGGTT TTTTGTGTTG CAAGCAGCAG  
4151 ATTACGCGCA GAAAAAAGG ATCTCAAGAA GATCCTTTGA TCTTTTCTAC  
4201 GGGGTCTGAC GCTCAGTGGG ACGAAAACCT ACGTTAAGGG ATTTTGGTCA  
4251 TGAGATTATC AAAAAGGATC TTCACCTAGA TCCTTTTAAA TAAAAAATGA  
4301 AGTTTAAAT CAATCTAAAG TATATATGAG TAAACTTGGT CTGACAGTTA  
4351 CCATGCTTA ATCAGTGAGG CACCTATCTC AGCGATCTGT CTATTTGTT  
4401 CATCCATAGT TGCTGACTC CCCGTCGTGT AGATAACTAC GATACGGGAG  
4451 GGCTTACCAT CTGGCCCCAG TGCTGCAATG ATACCGCGAG ACCCAGCTC  
4501 ACCGGCTCCA GATTTATCAG CAATAAACCA GCCAGCCGGA AGGGCCGAGC  
4551 GCAGAAGTGG TCCTGCAACT TTATCCGCCT CCATCCAGTC TATTAATTGT  
3826 4601 TGCCGGGAAG CTAGAGTAAG TAGTTCGCCA GTTAATAGTT TCGCAACGT  
4651 TCTTGCATTT GCTGCAGGCA TCGTGGTCTC ACGCTCGTCT TTTGGTATGG  
4701 CTTCATTCAG CTCCGCTTCC CAACGATCAA GGCGAGTTAC ATGATCCCCC

SUBSTITUTE SHEET

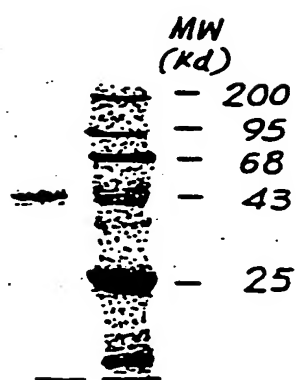
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*FIG. 22(cont'd)*

4751 ATGTTGTGCA AAAAAGCGGT TAGCTCCTTC GGTCCTCCGA TCGTTGTCAG  
4801 AAGTAAGTTG GCCGCAGTGT TATCACTCAT GGTTATGGCA GCACTGCATA  
4851 ATTCTCTTAC TGTCATGCCA TCCGTAAGAT GCTTTTCTGT GACTGGTGAG  
4901 TACTCAACCA AGTCATTCTG AGAATAGTGT ATGCGGCGAC CGAGTTGCTC  
4951 TTGCCCCGGCG TCAACACGGG ATAATACCGC GCCACATAGC AGAACTTTAA  
5001 AAGTGCTCAT CATTGGAAAA CGTTCTTCGG GCGGAAAAC CTCAAGGATC  
5051 TTACCGCTGT TGAGATCCAG TTCGATGTAA CCCACTCGTG CACCCAACTG  
5101 ATCTTCAGCA TCTTTTACTT TCACCAGCGT TTCTGGGTGA GCAAAAACAG  
5151 GAAGGCAAAA TGCCGCAAAA AAGGGAATAA GGGCGACACG GAAATGTTGA  
5201 ATACTCATAC TCTTCCTTTT TCAATATTAT TGAAGCATT ATCAGGGTTA  
5251 TTGTCTCATG AGCGGATACA TATTTGAATG TATTTAGAAA AATAAACAAA  
5301 TAGGGGTTCC GCGCACATTT CCCCAGAAAAG TGCCACCTGA CGTCTAAGAA  
5351 ACCATTATTA TCATGACATT AACCTATAAA AATAGGCGTA TCACGAGGCC  
5401 CTTTCGTCTT CAA

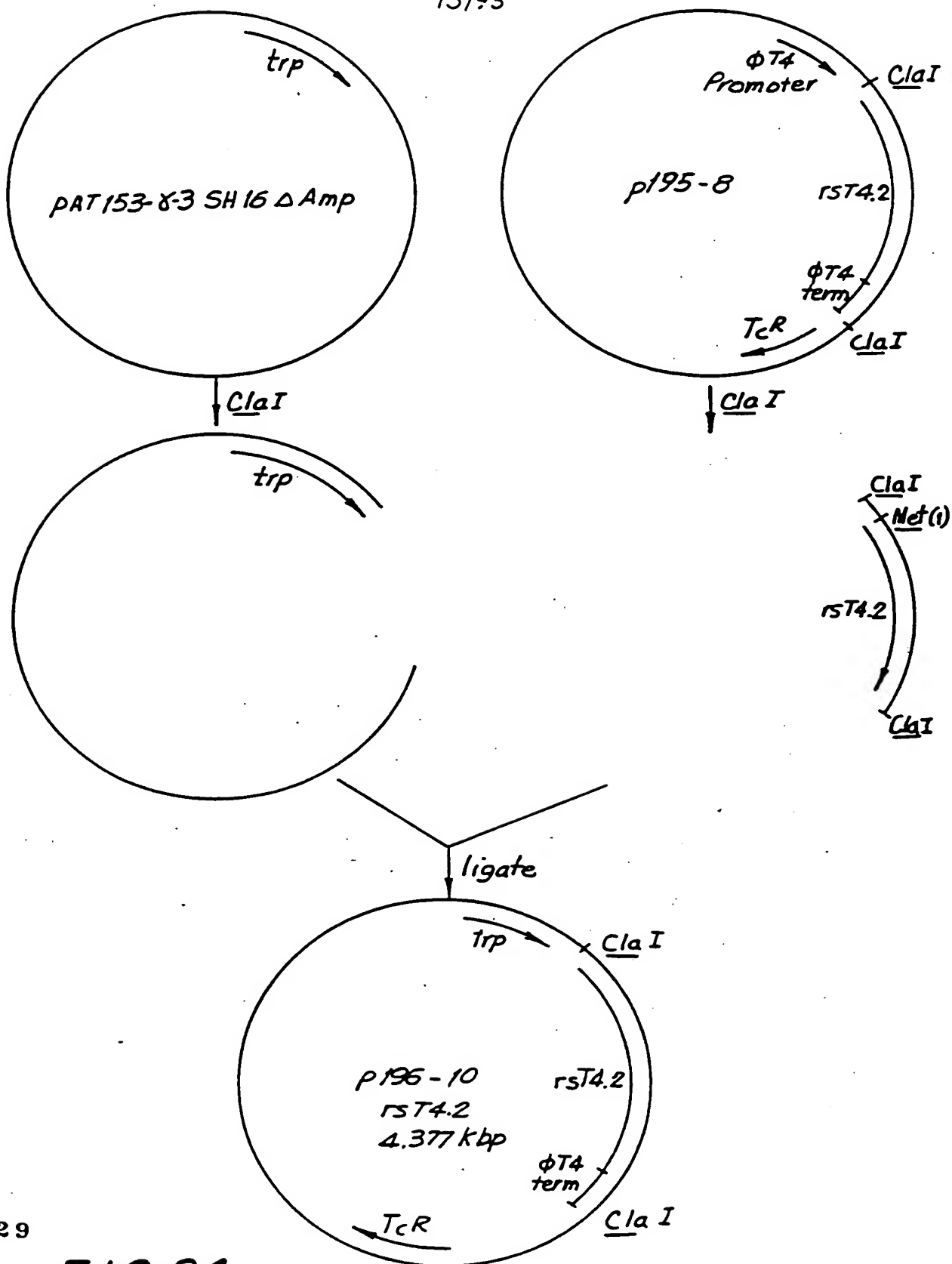
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*FIG. 23*





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FIG. 24

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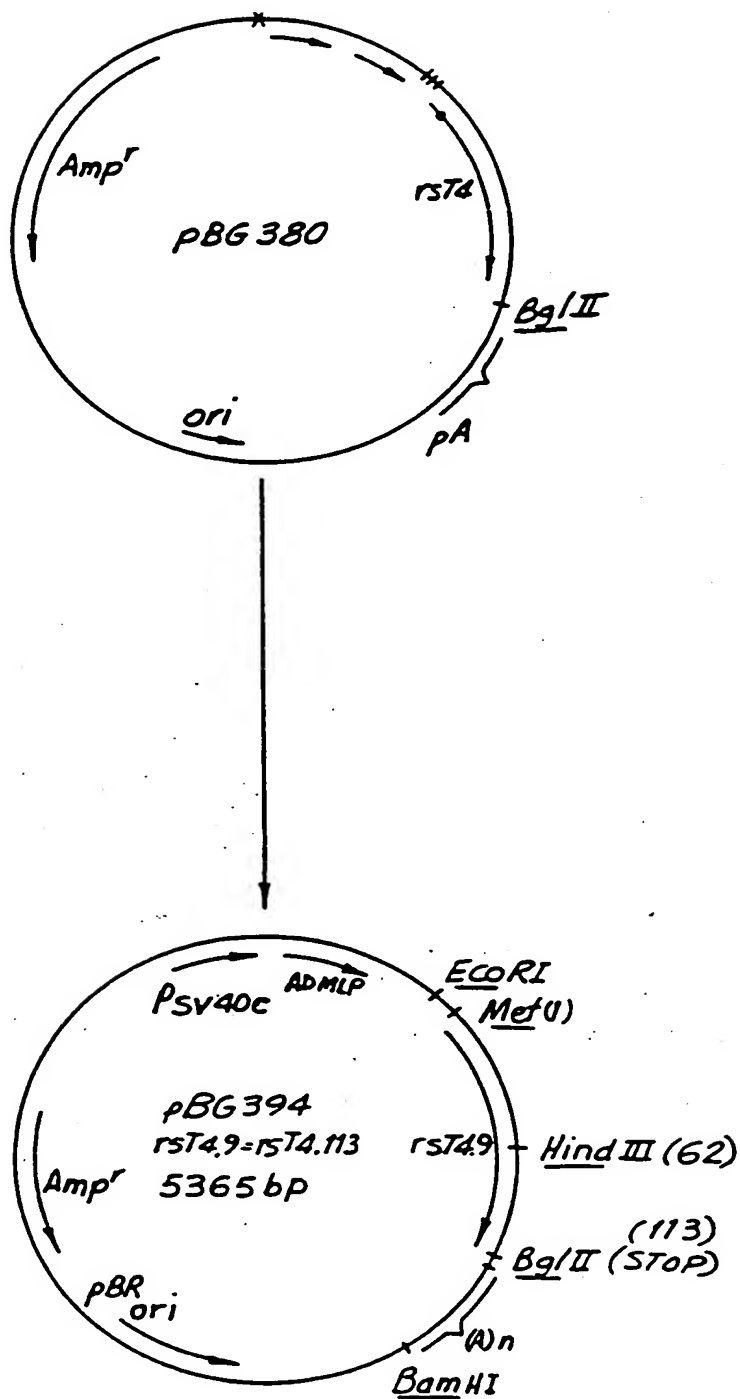


FIG.25

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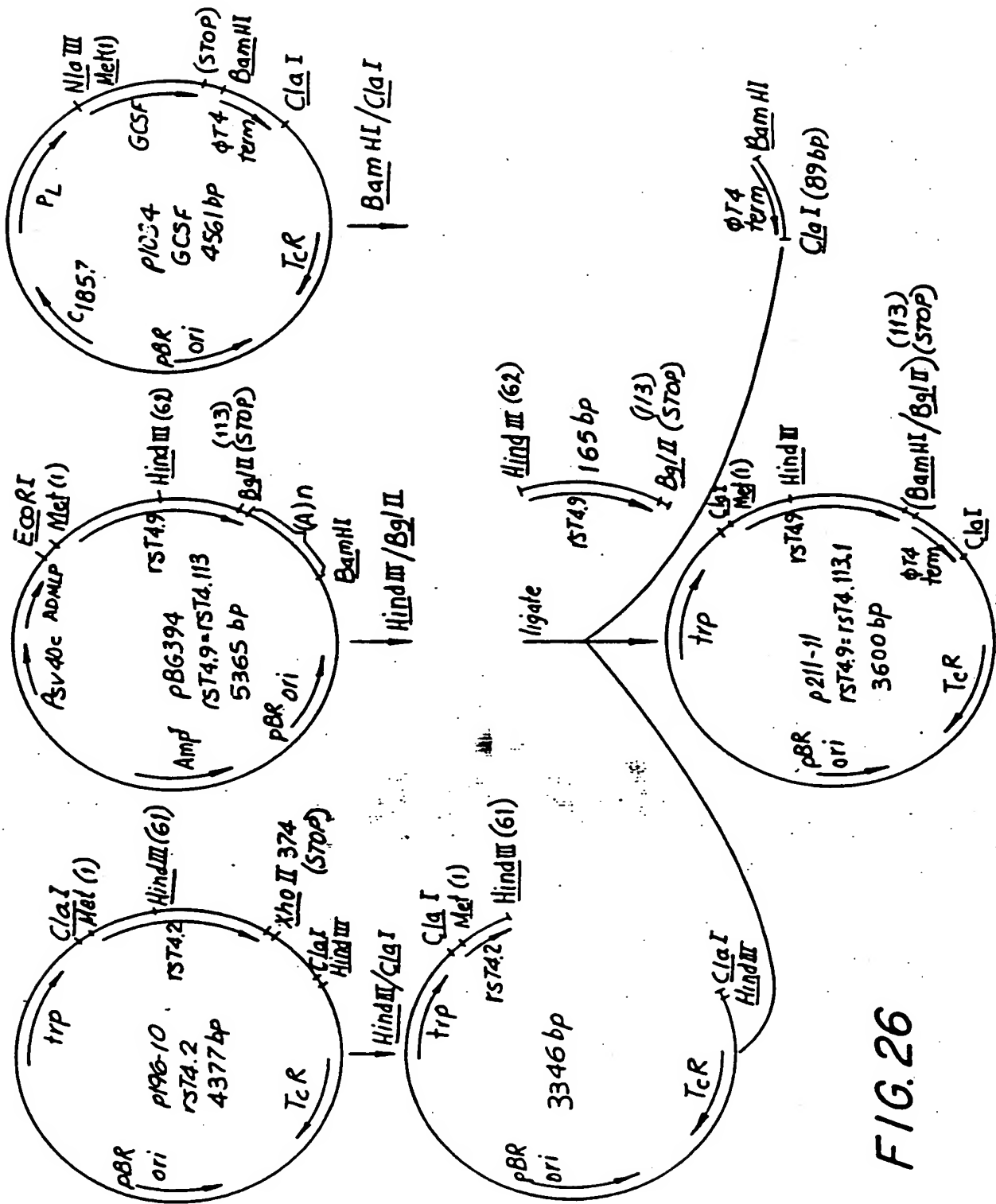


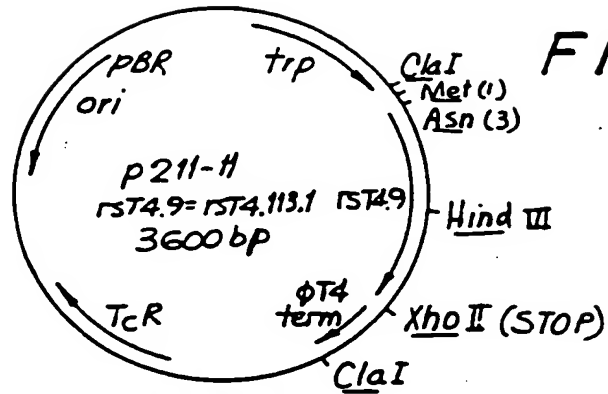
FIG. 26

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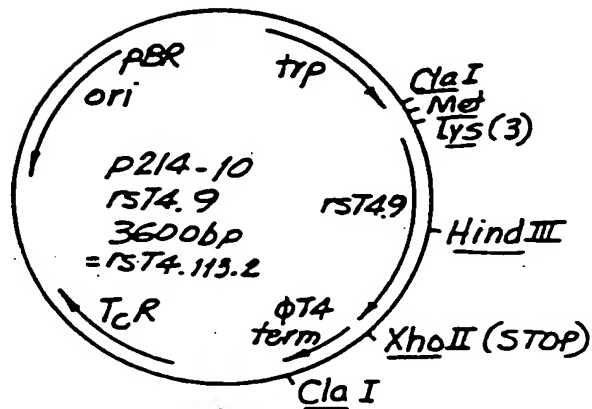
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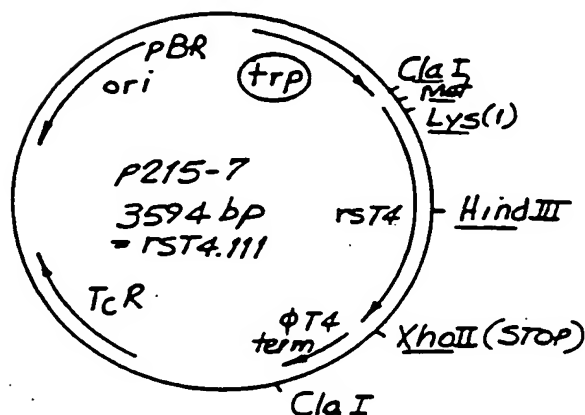
FIG. 27



Site directed mutagenesis  
to change an Asn at amino  
acid position #3 to a Lys,  
using T4-66

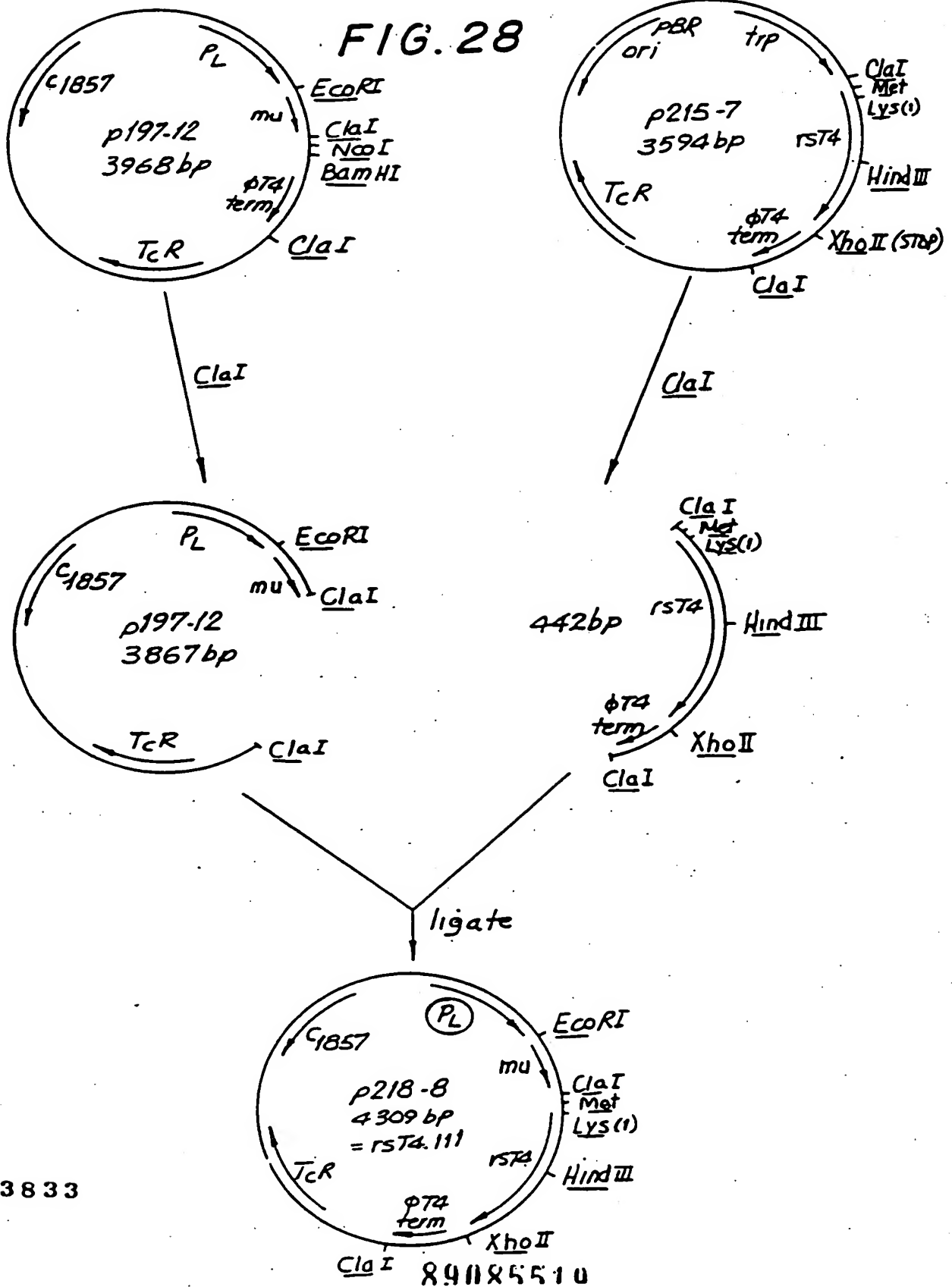


Site directed mutagenesis  
to delete Gln and Gly at  
amino acid positions #1, #2,  
using T4AID-87



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FIG. 28



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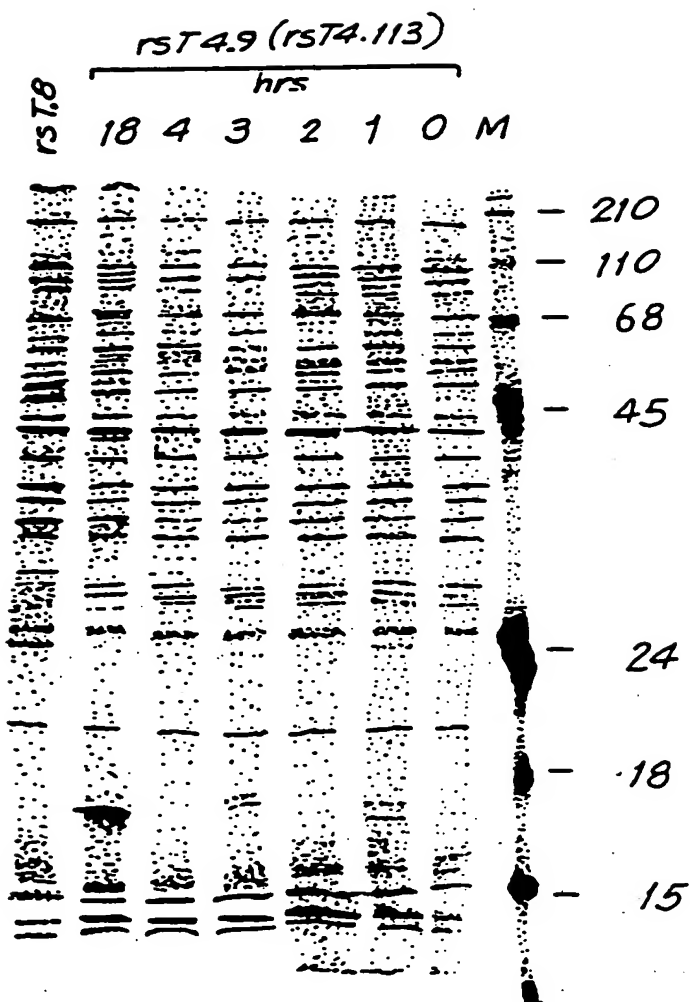


FIG. 29A

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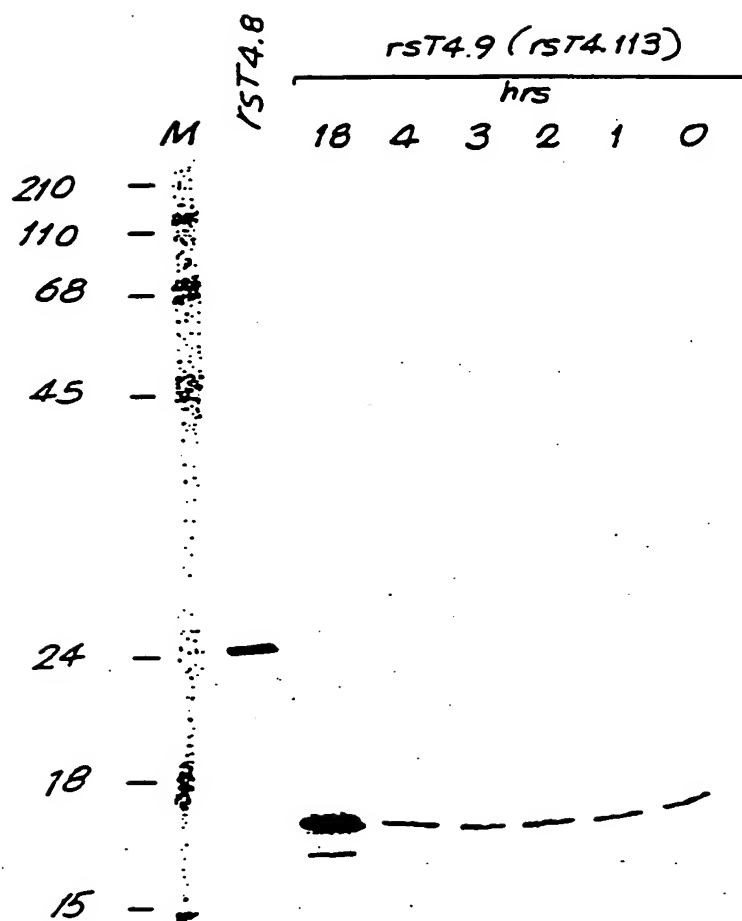
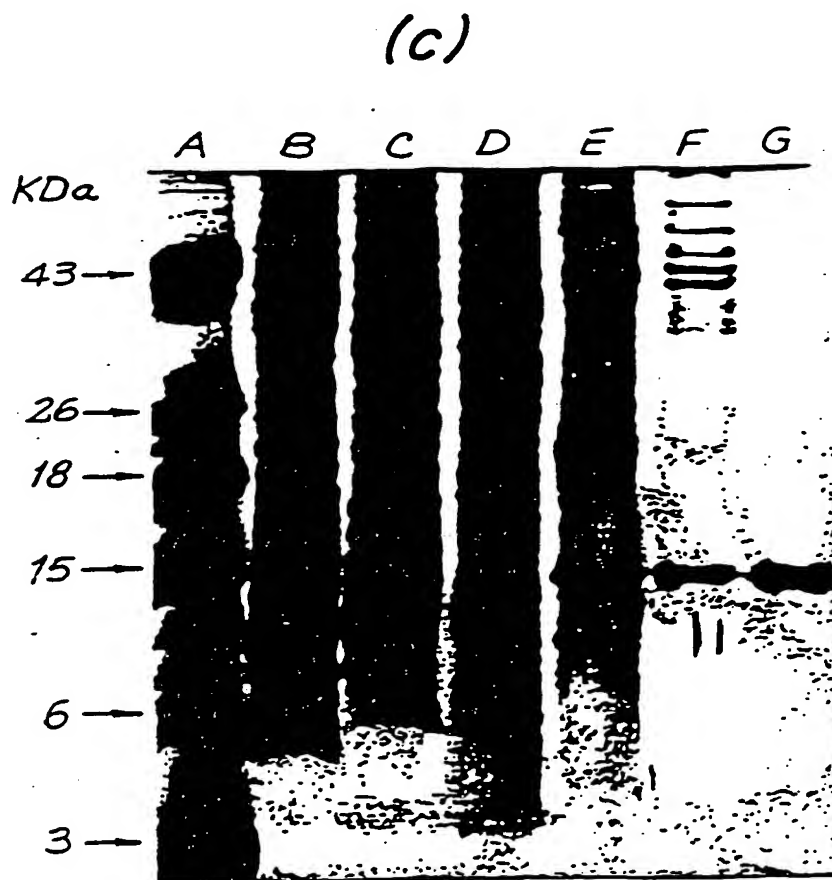
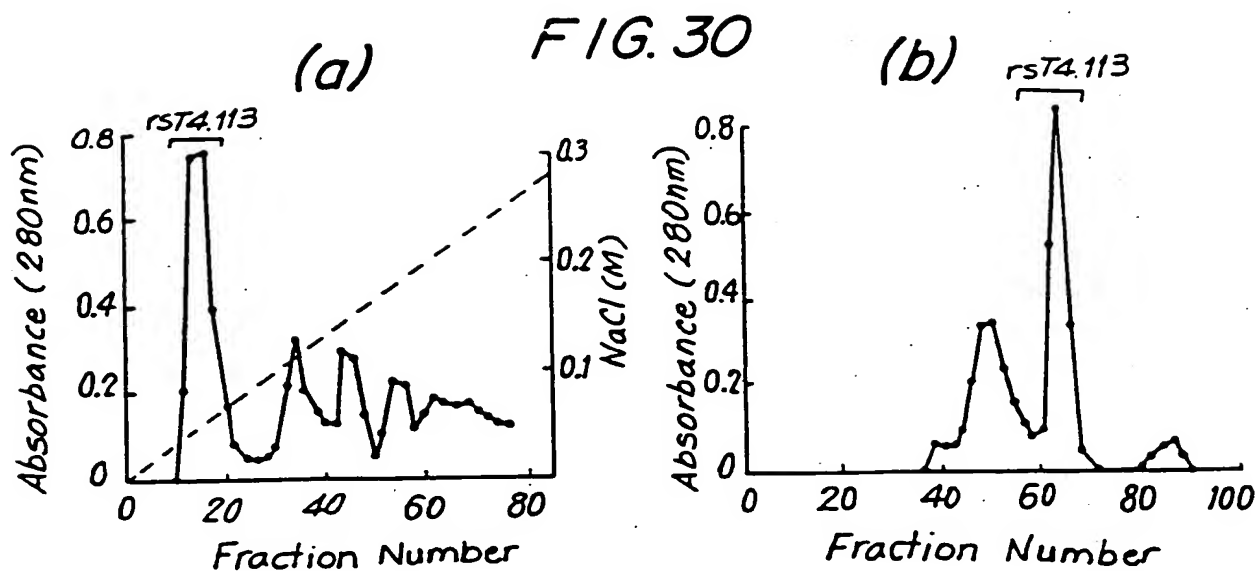


FIG. 29B

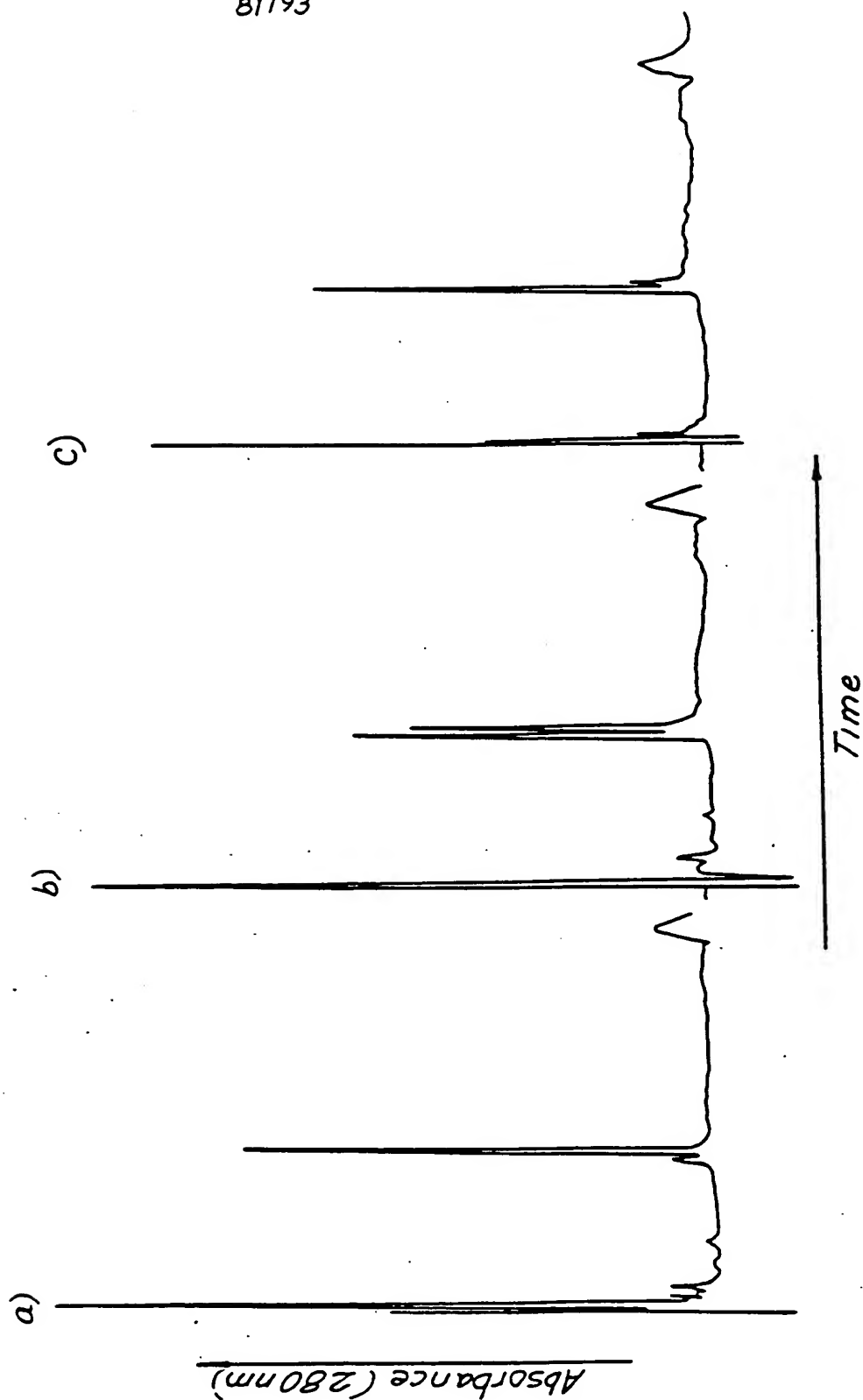
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FIG. 31



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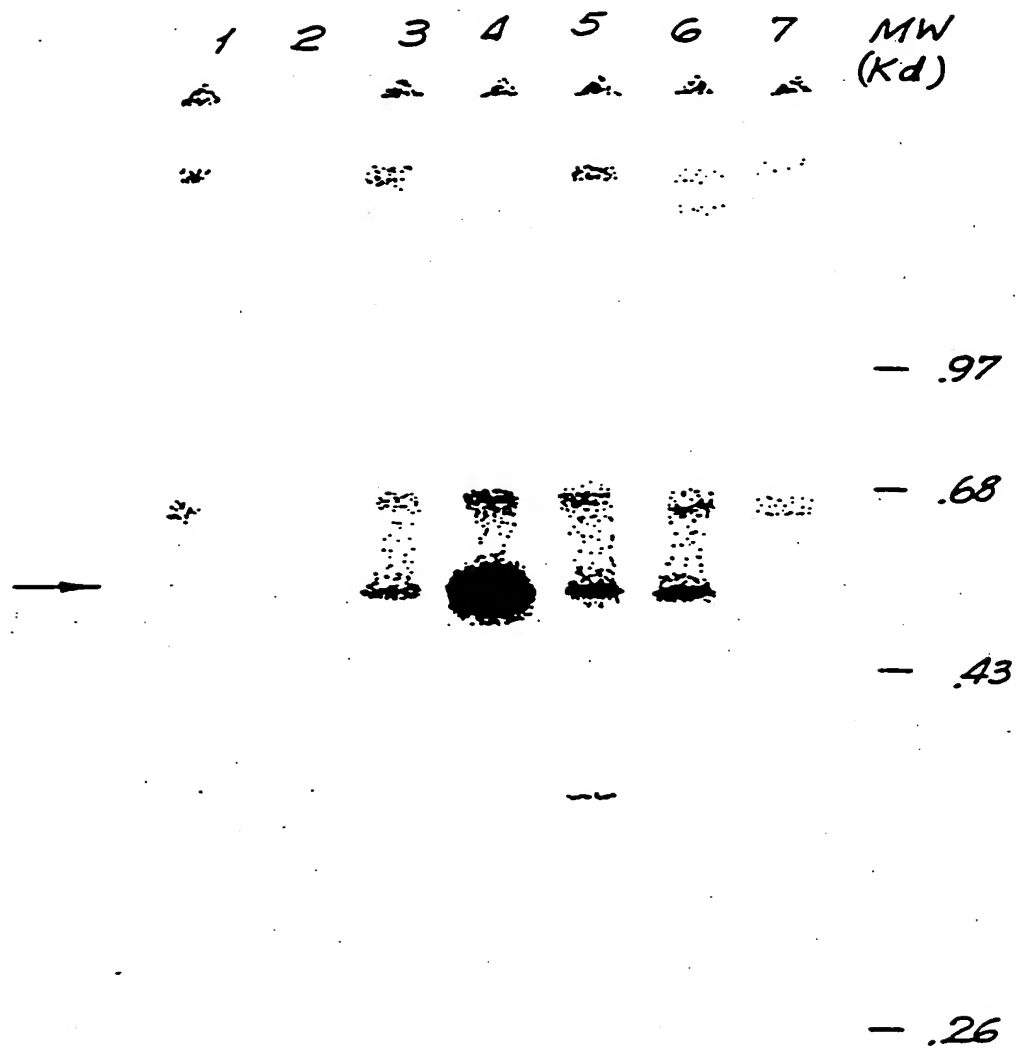
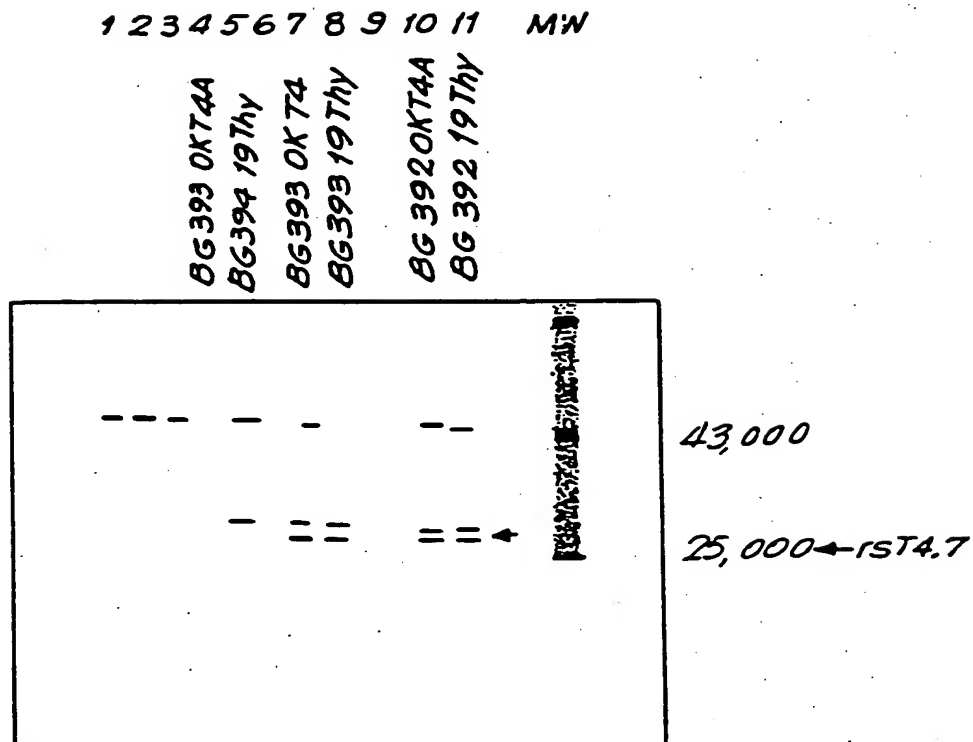


FIG. 32

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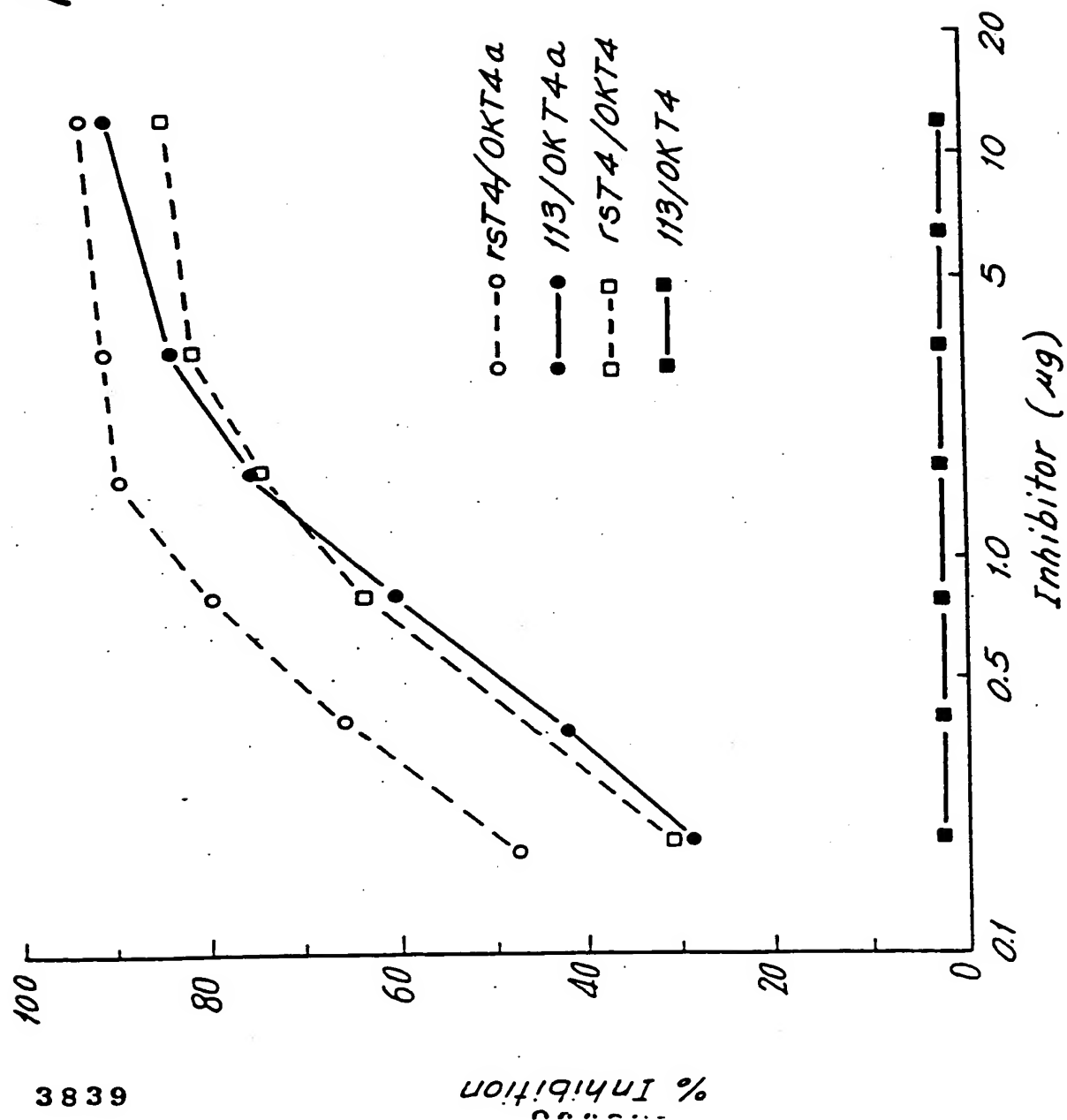


**FIG. 33**

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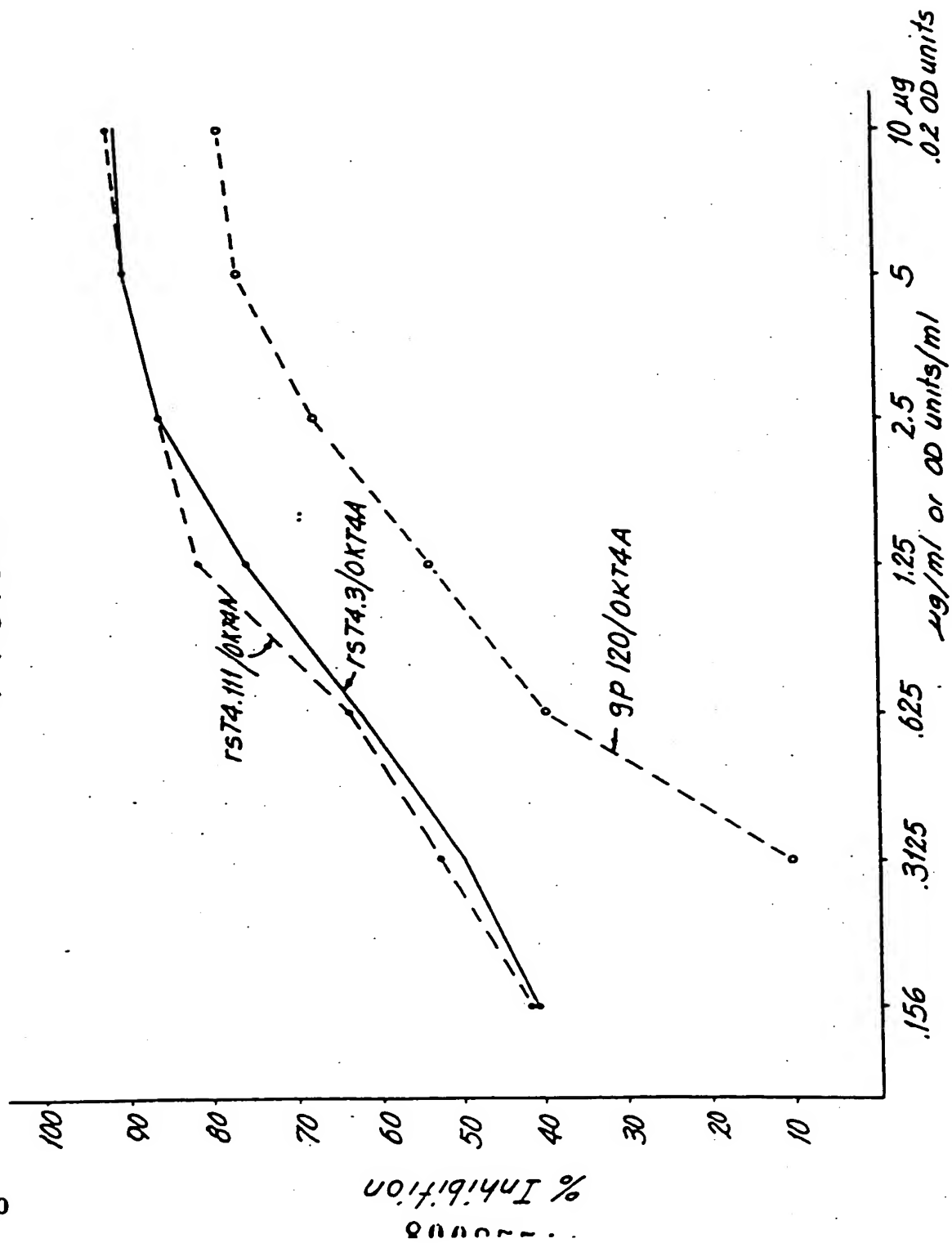
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FIG. 34



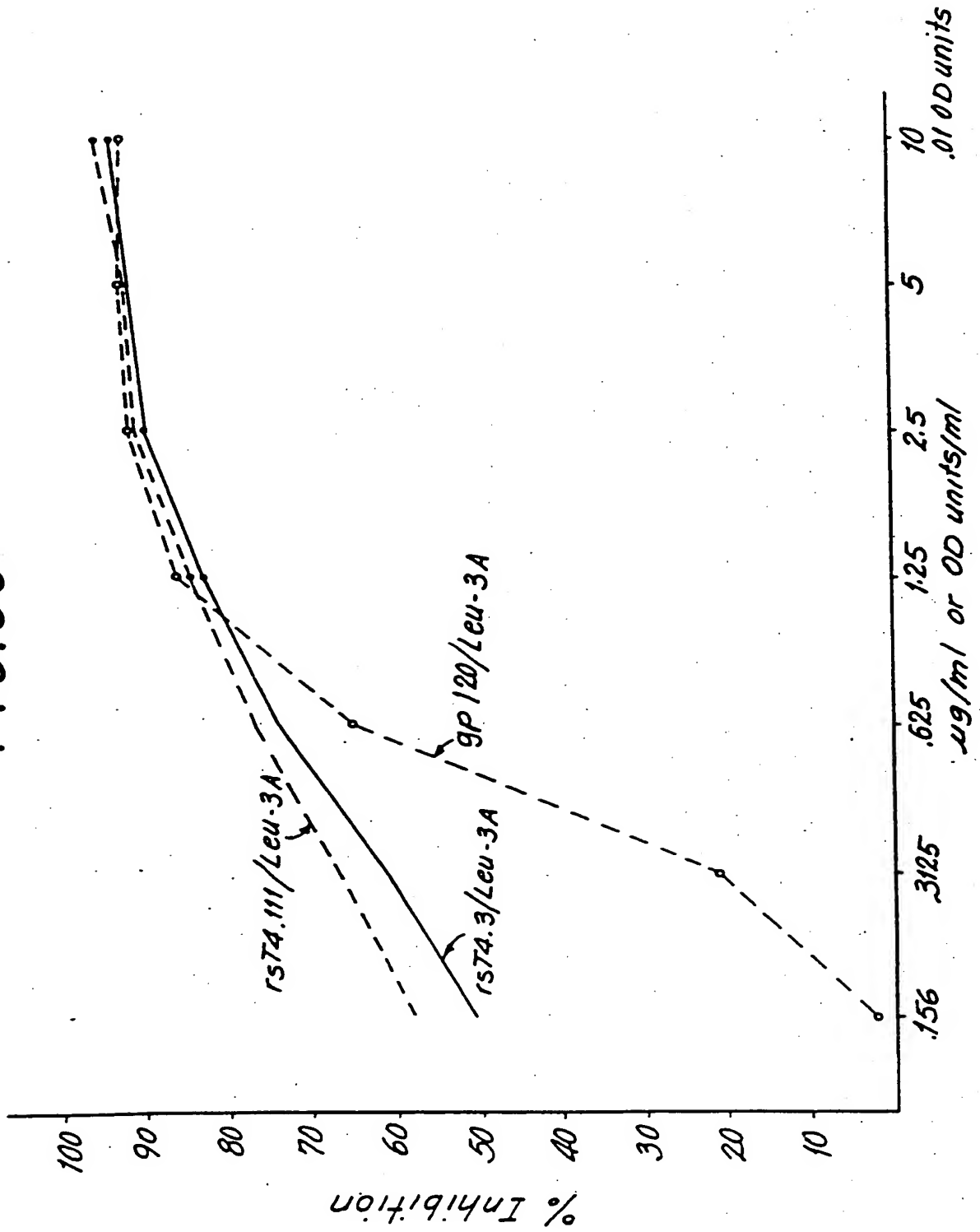
8:/93

FIG. 35



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FIG. 36

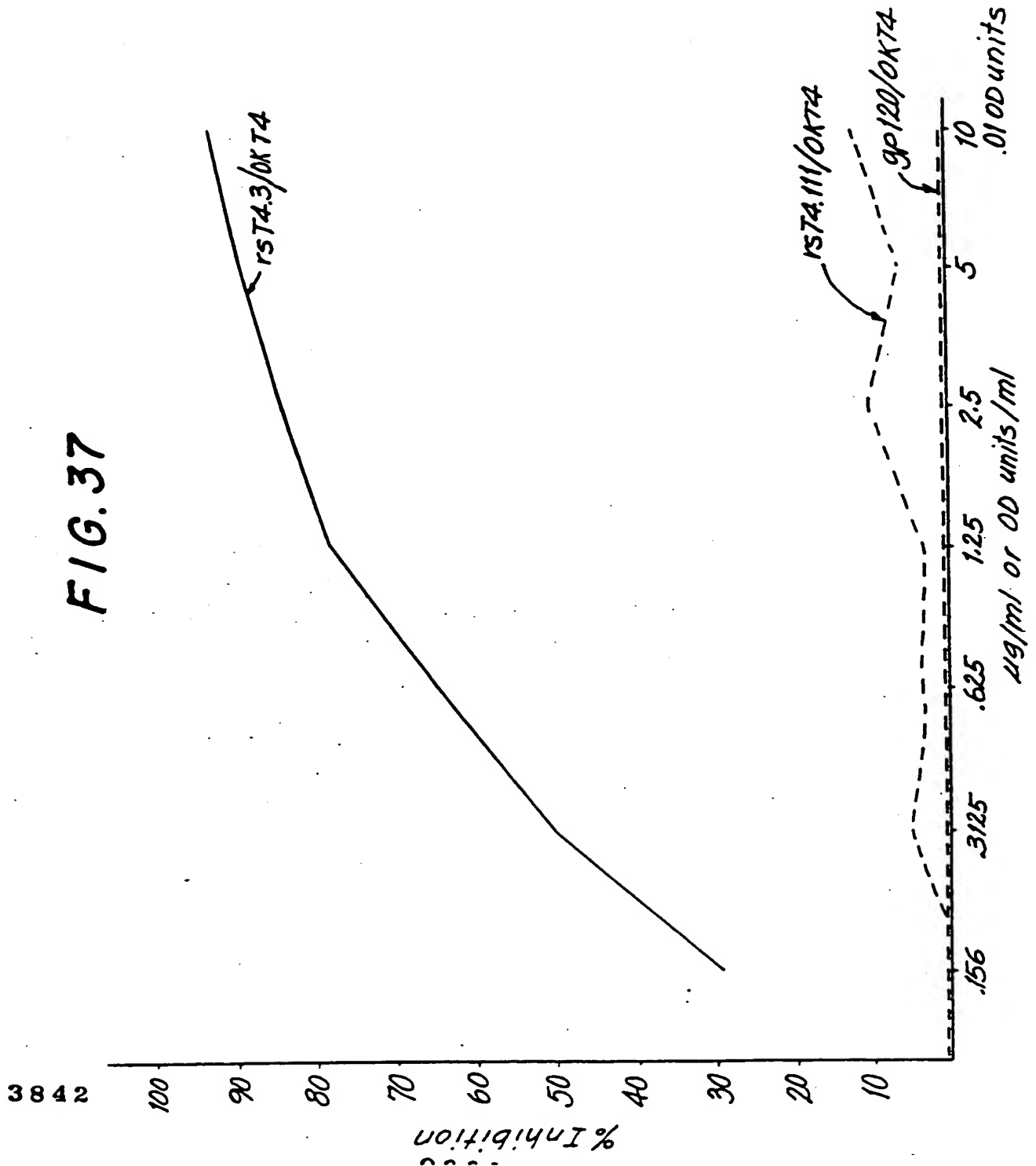


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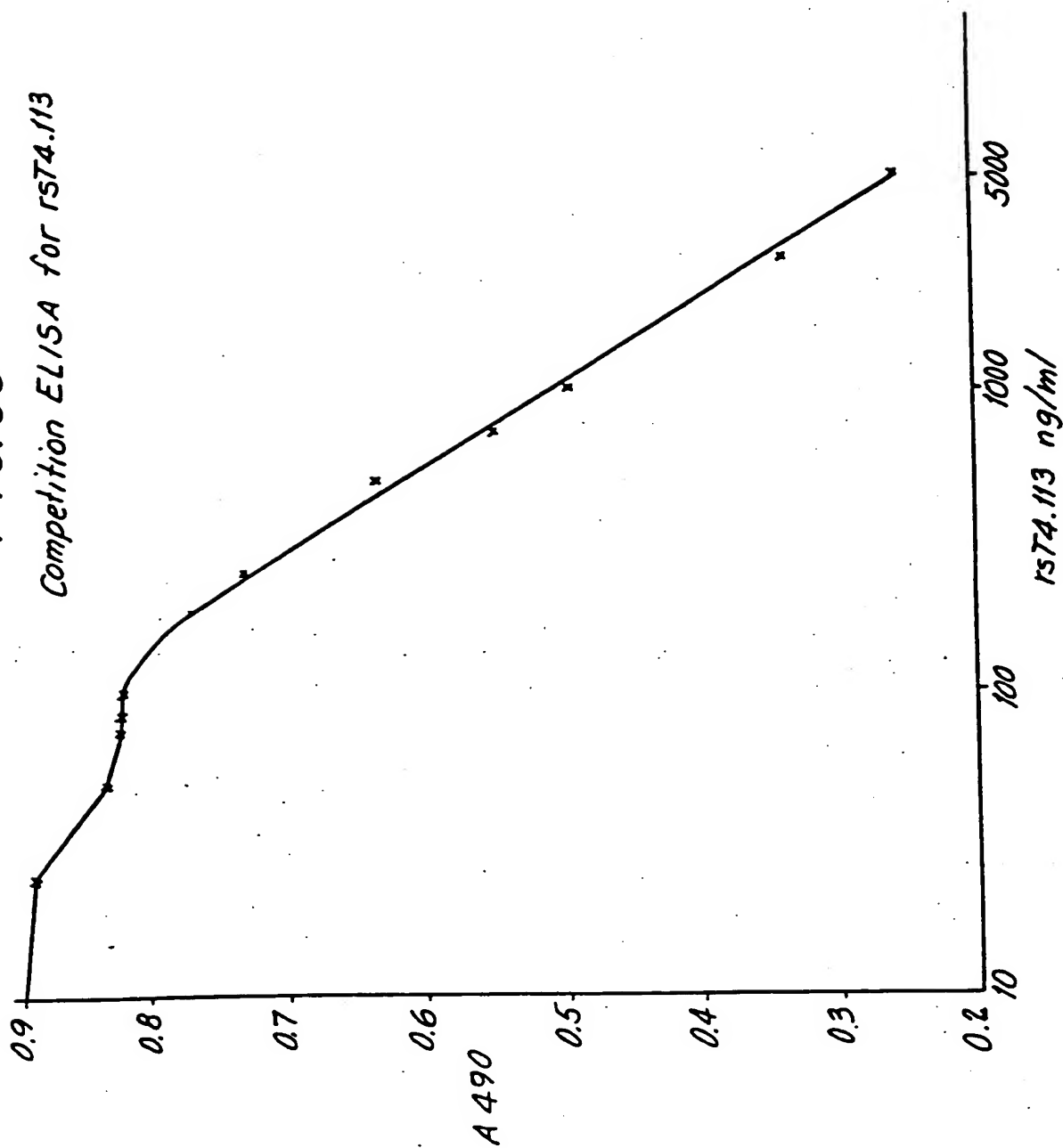
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FIG. 37



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**FIG. 38**  
*Competition ELISA for rsT4.113*



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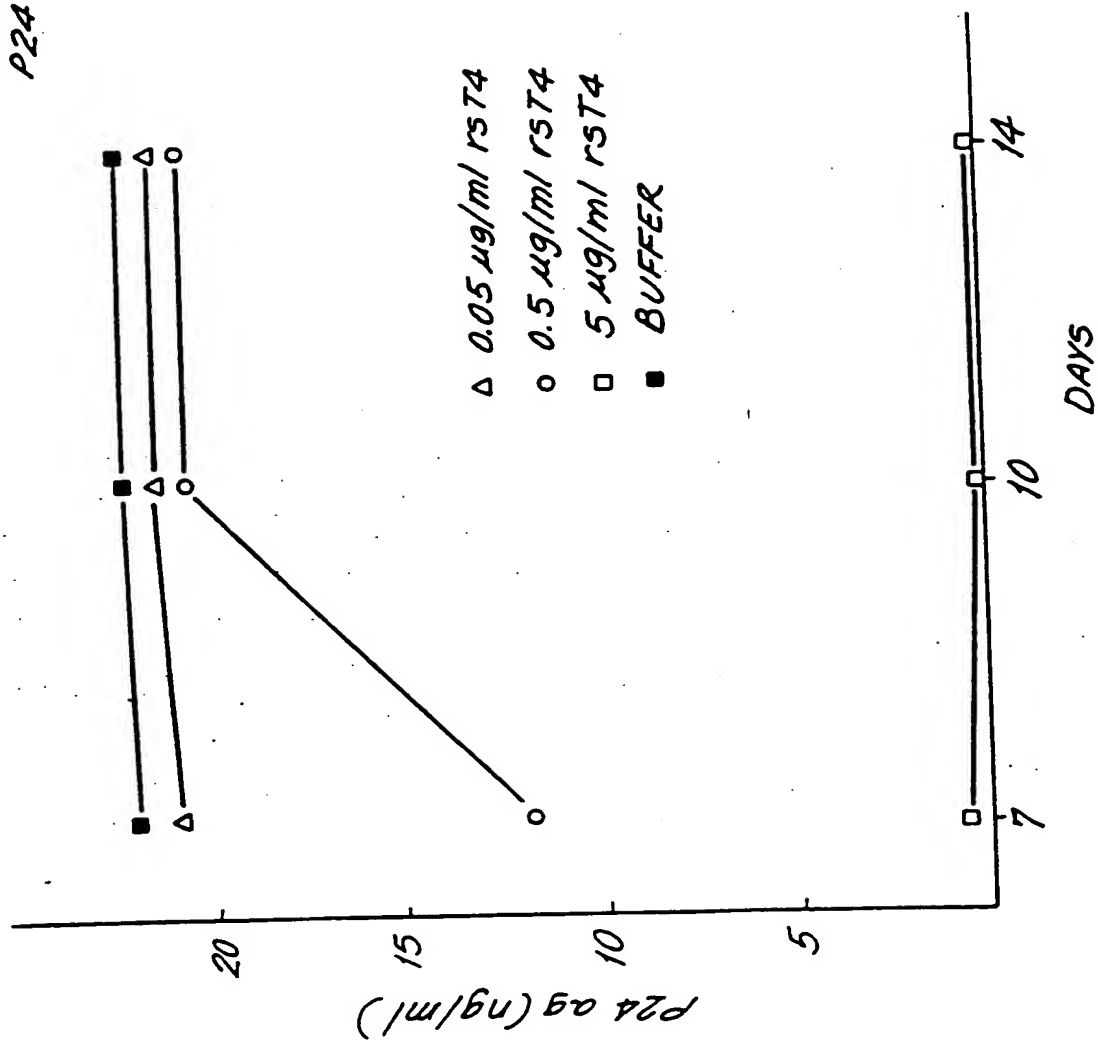
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FIG. 39

P24 ANTIGEN RIA

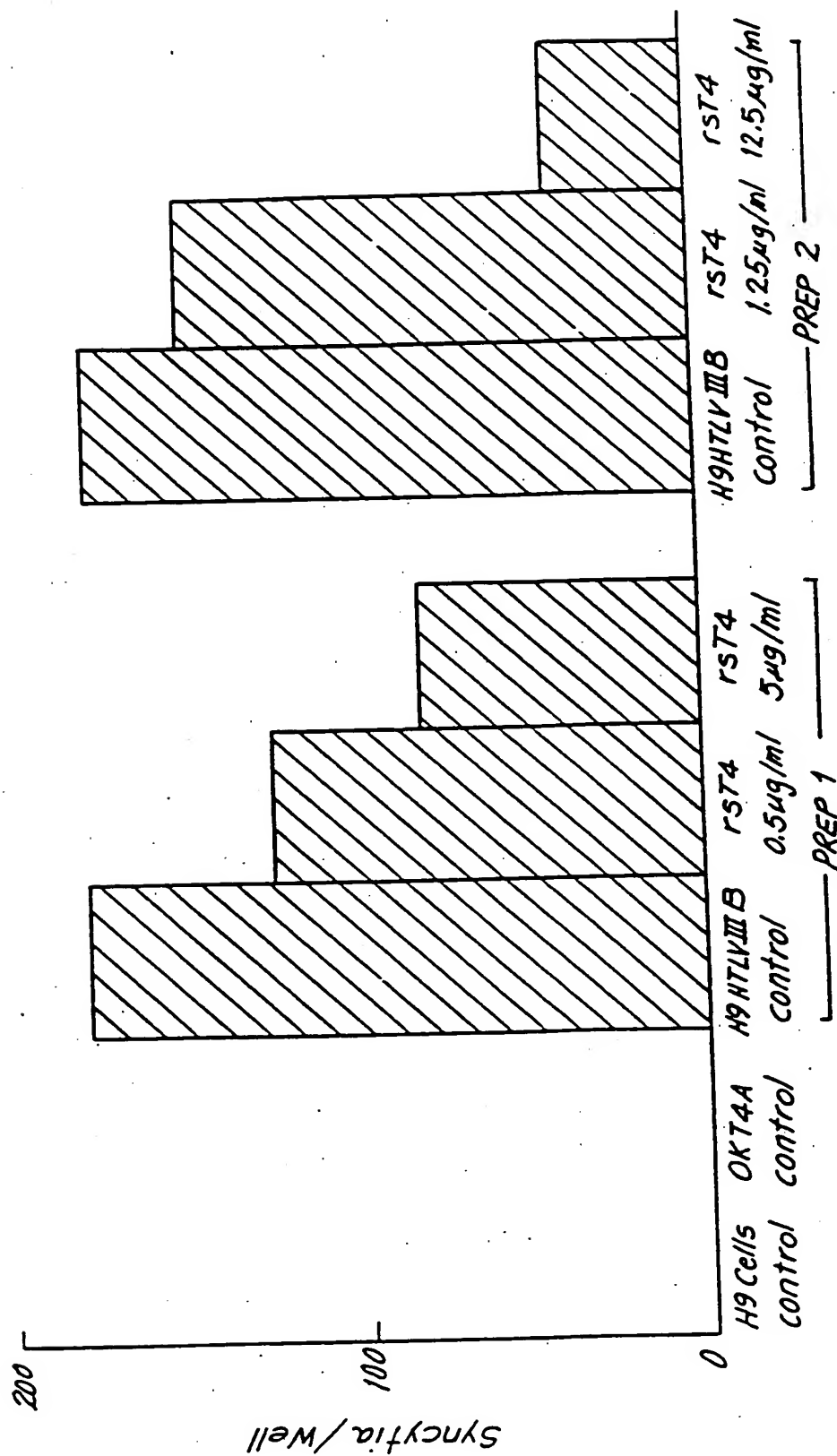


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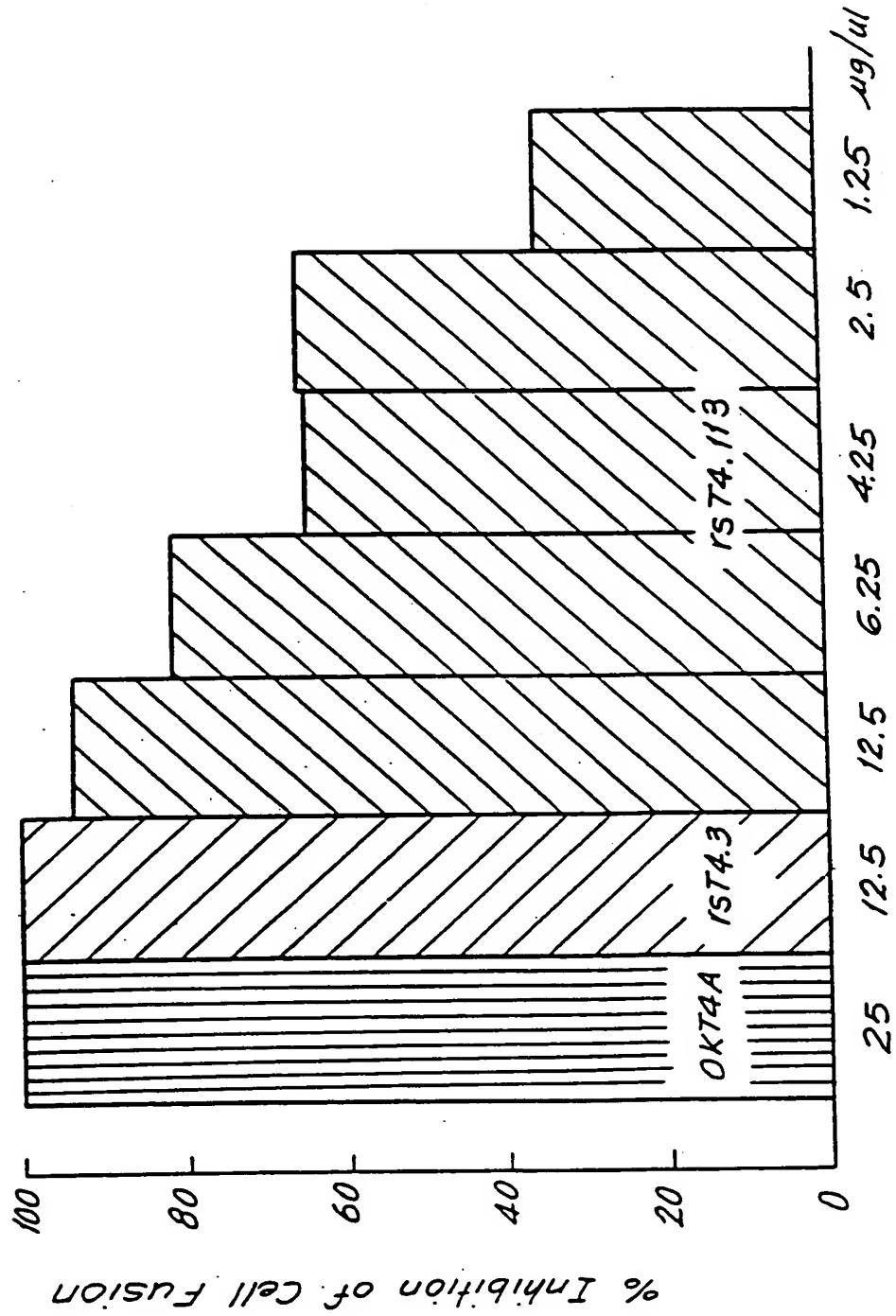
**FIG. 40**  
C8/66 CELL FUSION ASSAY



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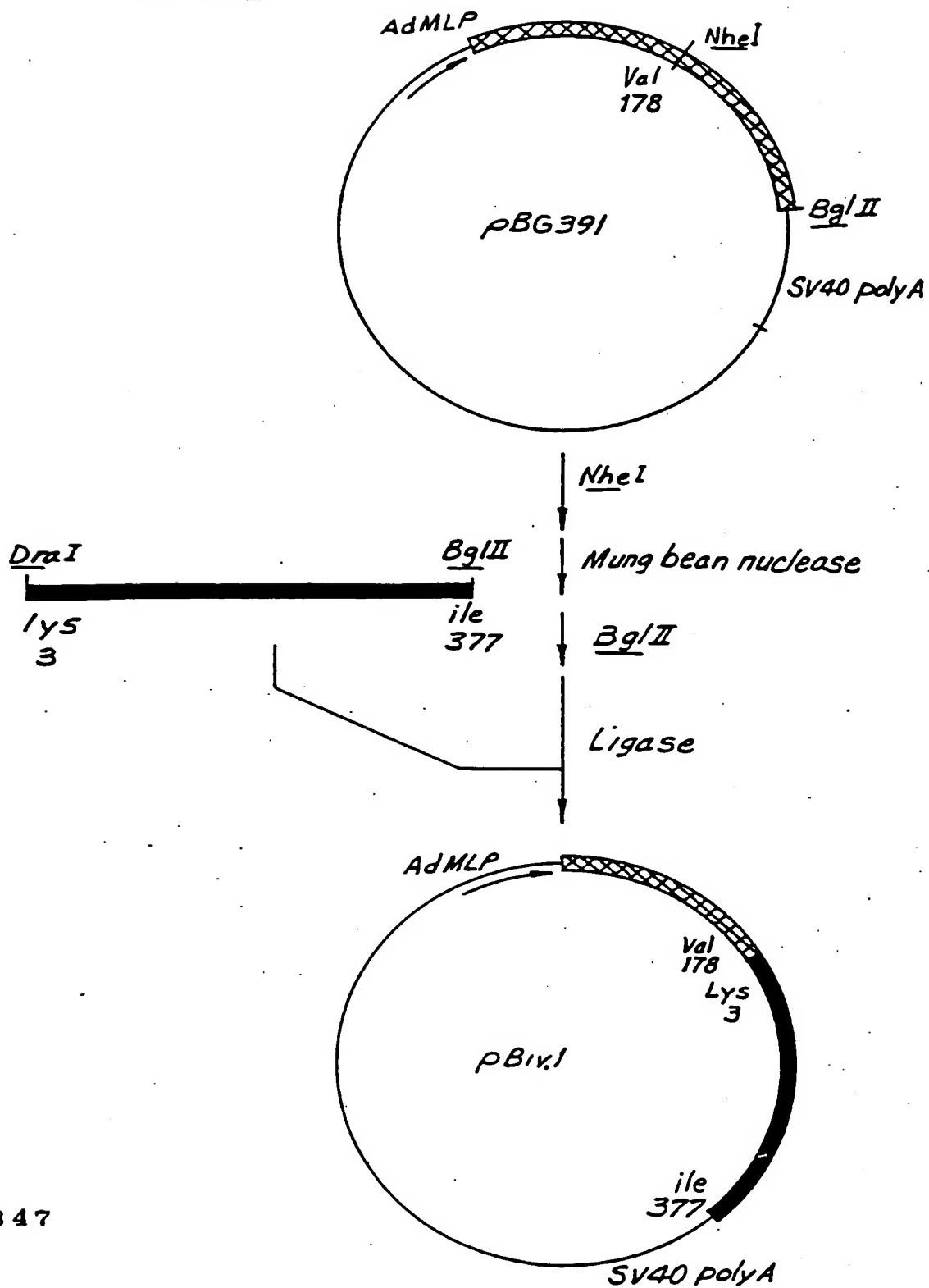
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FIG. 41



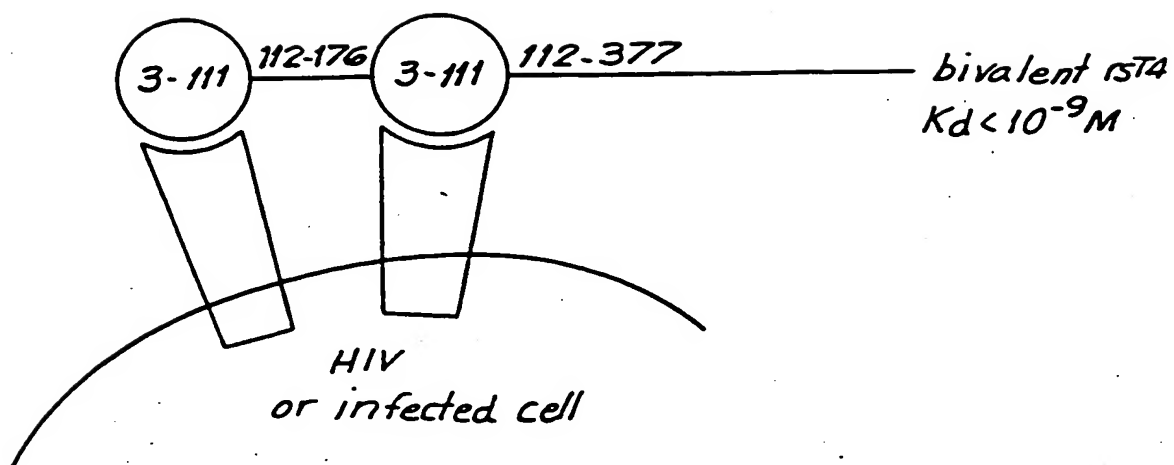
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FIG. 42



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**FIG. 43**

## MICROORGANISMS

Optional Sheet in connection with the microorganism referred to on page 95, lines 29-35 of the description:  
96, lines 19-21

## A. IDENTIFICATION OF DEPOSIT \*

96, lines 19-21

Further deposits are identified on an additional sheet ☒ -- 3 additional sheets attached

Name of depository institution \*

In Vitro International, Inc.

Address of depository institution (including postal code and country) \*

611 (P) Harmons  
 Ferry Road, Linthicum, Maryland 21090  
 United States of America

Date of deposit \*

See attached additional sheets

Accession Number \*

See attached additional sheets

B. ADDITIONAL INDICATIONS \* (Leave blank if not applicable). This information is continued on a separate attached sheet ☐

In respect of those designations in which a European patent is sought samples of the deposited microorganisms will be made available until the publication of the mention of the grant of the European patent or until the date on which the application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28(4) EPC).

C. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE \* (If the indications are not for all designated States)

D. SEPARATE FURNISHING OF INDICATIONS \* (Leave blank if not applicable)

The indications listed below will be submitted to the International Bureau later \* (Specify the general nature of the indications e.g., "Accession Number of Deposit")

E. ☐ This sheet was received with the international application when filed (to be checked by the receiving Office)

(Authorized Officer)

☐ The date of receipt (from the applicant) by the International Bureau is:

13 JANUARY 1989  
 (13. 01. 89)

(Authorized Officer)

(January 1985)

Additional Sheet 1 of 3 To Form  
PCT/RO/134

Continuation Of Box A

IDENTIFICATION OF DEPOSITS

BG378: E.coli MC1061/pBG378  
199-7: E.coli MC1061/p199-7  
170-2: E.coli JA221/p170-2  
EC100: E.coli JM83/pEC100  
BG377: E.coli MC1061/pBG377  
BG380: E.coli MC1061/pBG380  
BG381: E.coli MC1061/pBG381

DATE OF DEPOSITS

2 September 1987

ACCESSION NUMBERS

IVI 10143  
IVI 10144  
IVI 10145  
IVI 10146  
IVI 10147  
IVI 10148  
IVI 10149

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Additional Sheet 2 of ~ To Form  
PCT/RO/134

Continuation Of Box A

IDENTIFICATION OF DEPOSITS

BG-391:	<u>E.coli</u>	MC1061/pBG391
BG-392:	<u>E.coli</u>	MC1061/pBG392
BG-393:	<u>E.coli</u>	MC1061/pBG393
BG-394:	<u>E.coli</u>	MC1061/pBG394
BG-396:	<u>E.coli</u>	MC1061/pBG396
203-5:	<u>E.coli</u>	SG936/p203-5

DATE OF DEPOSITS

6 January 1988

ACCESSION NUMBERS

IVI 10151
IVI 10152
IVI 10153
IVI 10154
IVI 10155
IVI 10156

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Additional Sheet 3 of 3 To Form  
PCT/RO/134

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Continuation Of Box A

IDENTIFICATION OF DEPOSITS

211-11: E.coli A89/pBG211-11  
214-10: E.coli A89/pBG214-10  
215-7: E.coli A89/pBG215-7

DATE OF DEPOSITS

24 August 1988

ACCESSION NUMBERS

IVI 10183  
IVI 10184  
IVI 10185

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# INTERNATIONAL SEARCH REPORT

International Application No. PCT/US88/02940

**I. CLASSIFICATION OF SUBJECT MATTER** (if several classification symbols apply, indicate all)<sup>a</sup>  
 According to International Patent Classification (IPC) or to both National Classification and IPC  
 IPC(4): C07H 15/12; C12Q 1/70, C12Q 1/02, see attachment.  
 U.S. CL.: 536/27; 435/5,29,39,68,91,170,172.3, see attachment

**II. FIELDS SEARCHED**

Minimum Documentation Searched<sup>b</sup>

Classification System	Classification Symbols
U.S.	435/5,29,39,68,91,170,172.1,172.3,240,253,320; 530/350,412; 514/2; 424/85; 536/27; 955/6, 9, 11,12,15,22,23,24,59,60,65,66

Documentation Searched other than Minimum Documentation  
 to the Extent that such Documents are Included in the Fields Searched<sup>c</sup>

Chemical Abstract Data Base (CAS) 1967-1988; Biosis Data Base 1969-1988 Keywords: CD4, T4, TCell, AIDS, HTLV, HTLVI, HTLVIII, see attachment.

**III. DOCUMENTS CONSIDERED TO BE RELEVANT<sup>d</sup>**

Category <sup>e</sup>	Citation of Document, " with indication, where appropriate, of the relevant passages <sup>f</sup>	Relevant to Claim No. <sup>g</sup>
Y	SCIENCE, Volume 234, issued 1986 November, (Washington, DC., U.S.A.), (O.J. SATTENTAU ET AL), "Epitopes of the CD4 Antigen and HIV Infection" See pages 1120-1123. See particularly page 1120	13-20, 29-33 and 48-52
Y	SCIENCE, Volume 234, issued 1986, November, (Washington, D.C. U.S.A) (J.A. HOXIE ET AL), "Alterations in T4 (CD4) Protein and mRNA synthesis in Cells Infected with HIV" see pages 1123-1127. See particularly page 1123.	13-20, 29-33, and 48-52
Y,P	PROCEEDINGS NATIONAL ACADEMY OF SCIENCES, U.S.A, Volume 84, issued 1987 December (Washington, D.C., U.S.A), (P.J. MADDON ET AL.), "Structure and Expression of the Human and Mouse T4 Genes", See pages 9155-9159, See particularly page 9155 and 9156.	1-4, 25-27, 34-36 and 39-46

<sup>a</sup> Special categories of cited documents:

- "A" document defining the general state of the art which is not considered to be of particular relevance
- "E" earlier document but published on or after the international filing date
- "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- "O" document referring to an oral disclosure, use, exhibition or other means
- "P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

**IV. CERTIFICATION**

Date of the Actual Completion of the International Search

Date of Mailing of this International Search Report

20 NOVEMBER 1988

03 FEB 1989

International Searching Authority

ISA/US

Signature of Authorizing Officer  
 Richard C. Pett  
 RICHARD C. PETT

Attachment to PCT/ISA/210  
I. Classification of Subject Matter

IPC: C12Q 1/06, C12P 21/00, C12P 19/34, C12P 1/04, C12N  
15/00, C12N 7/00; C07K 13/00, C07K 3/00; A61K  
37/68; A61K 39/00, A61K 45/02

US.CL.: 240, 320; 530/350, 412; 514/2; 424/85

II. Fields Searched

Keywords: ARC, Surface, receptor, therap?, purifi?,  
Immunoassay, Detection, Pharmaceutical Composition,  
Lymphocyte, Igg, Polyvalent, Solub?, gene, Clon?, Protein,  
Polypeptide, Fusion, Expression, Vector, Plasmid, Surface  
Protein, Surface Antigen, Acquired Immune Deficiency  
Syndrome, Retrovirus

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## III DOCUMENTS CONSIDERED TO BE RELEVANT (CONTINUED FROM THE SECOND SHEET)

Category	Citation of Document, with indication, where appropriate, of the relevant passages	Relevant to Claim No
Y	<u>PROCEEDINGS NATIONAL ACADEMY OF SCIENCES, U.S.A.</u> Volume 84, issued 1987, June (Washington, D.C., U.S.A.), (T.C. CHANH ET AL.), "Monoclonal Anti-idiotypic Antibody Mimics the CD4 Receptor and Binds Human Immunodeficiency Virus" See pages 3891-3895. See particularly page 3891.	13-24, 29-33 and 48-52
X Y	<u>CELL</u> , Volume 47, issued 1986, November, (Cambridge, Mass., U.S.A) (P.J. MADDON ET AL.), "The T4 Gene Encodes the AIDS Virus Receptor and is Expressed in the Immune System and the Brain", See pages 333-348, See particularly pages 333-335.	1,3-6 and 25-27 2,7-24 and 28-50
P, Y	<u>CHEMICAL ABSTRACTS</u> , Volume 107, no. 15, issued 1987 October 12 (Columbus, Ohio, U.S.A), T.L. LENTZ et al, "Rabies virus binding to cellular membranes measured by enzyme immunoassay" see page 359, column 1, the abstract no. 131853i, Muscle Nerve, 1985, 8(4), 336-345 (Eng).	16-18 32-33 and 50
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